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OM protein - protein search, using sw model

Run on: July 8, 2005, 14:10:22 ; Search time 27 Seconds
(without alignments)
1340.918 Million cell updates/sec

Title: US-10-690-991-2

Perfect score: 2542

Sequence: 1 MARGTHSHGLFKKLGIRGPT.....PVLKVESRDGTSGAHHH 485

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2501	98.4	508	4	US-09-949-016-7092
2	2501	98.4	508	4	US-09-949-016-8562
3	2494	98.1	503	4	US-09-144-367-2
4	2233	87.8	508	4	US-09-949-016-8561
5	2142.5	84.3	502	4	US-09-949-016-5992
6	2142.5	84.3	507	4	US-09-949-016-7091
7	1957	77.0	503	4	US-09-583-447A-2
8	1946.5	76.6	504	4	US-08-457-274A-25
9	1946.5	76.6	504	4	US-09-583-447A-4
10	1946.5	76.6	504	5	PCT-US95-05758-25
11	1620	63.7	420	4	US-09-583-447A-6
12	840.5	33.1	554	4	US-09-949-016-11161
13	840.5	33.1	554	4	US-09-949-016-11162
14	802	31.5	250	4	US-09-583-447A-8
15	721.5	28.4	529	4	US-09-270-767-46468
16	671	26.4	507	1	US-08-457-274A-22
17	671	26.4	507	1	PCT-US95-05758-22
18	643	25.3	526	1	US-08-298-426-4
19	630	24.8	498	1	US-08-457-274A-24
20	630	24.8	498	5	PCT-US95-05758-24
21	621.5	24.4	507	1	US-08-457-274A-23
22	621.5	24.4	507	5	PCT-US95-05758-23
23	591	23.2	517	1	US-08-457-274A-2
24	591	23.2	517	5	PCT-US95-05758-2
25	588	23.1	517	1	US-08-457-274A-28
26	588	23.1	517	5	PCT-US95-05758-28
27	569.5	22.4	1023	4	US-09-270-767-43827

28	518.5	20.4	372	4	US-09-270-767-33357	Sequence 3357, A
29	518.5	20.4	372	4	US-09-270-767-48574	Sequence 48574, A
30	428.5	16.9	510	4	US-09-852-067-2	Sequence 2, Appl
31	426	16.8	524	4	US-09-976-594-533	Sequence 533, App
32	425	16.7	512	4	US-09-270-767-45399	Sequence 45399, A
33	423.5	16.7	245	4	US-09-270-767-43855	Sequence 43855, A
34	416.5	16.4	520	4	US-09-949-016-6003	Sequence 6003, Ap
35	416.5	16.4	527	4	US-09-949-016-10078	Sequence 10078, A
36	416	16.4	520	4	US-09-527-073-2	Sequence 2, Appl
37	415.5	16.3	576	3	US-08-948-564-16	Sequence 16, Appl
38	410.5	16.1	489	3	US-09-852-067-4	Sequence 4, Appl
39	409	16.1	508	3	US-09-111-730-2	Sequence 2, Appl
40	409	16.1	508	4	US-09-949-016-5994	Sequence 5994, Ap
41	409	16.1	523	4	US-09-949-016-10466	Sequence 10466, A
42	401	15.8	500	4	US-09-949-016-7973	Sequence 7973, Ap
43	400	15.7	476	1	US-08-313-075A-30	Sequence 30, Appl
44	394	15.5	557	3	US-09-518-386B-1	Sequence 1, Appl
45	394	15.5	557	3	US-09-518-386B-3	Sequence 3, Appl

ALIGNMENTS

```
RESULT 1
US-09-949-016-7092
; Sequence 7092, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTUR, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OR INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 7092
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7092

Query Match      98.4%; Score 2501; DB 4; Length 508;
Best Local Similarity 100.0%; Pred. No. 3.4e-244;
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	3	YGHSHGLFKKLGIRGPTLPPLFGNITLSYHKGCMFDMCHKKYGVKGFYDQOQVLA	62
DB	30	YGHSHGLFKKLGIRGPTLPPLFGNITLSYHKGCMFDMCHKKYGVKGFYDQOQVLA	89
QY	63	TDDPMIKTVLVKCVFTNRBPFGVGFPMKSAISIAEDBEMRLSLSPFTSGLKE	122
DB	90	TDDPMIKTVLVKCVFTNRBPFGVGFPMKSAISIAEDBEMRLSLSPFTSGLKE	149
QY	123	MVPIIQYGVVLRNRRRRETKPKVTLKDVPRAYSMVYTSFVNIDSLNPPDPV	182
DB	150	MVPIIQYGVVLRNRRRRETKPKVTLKDVPRAYSMVYTSFVNIDSLNPPDPV	209
QY	183	ENFKKLRFDPFLDPFLSTVFPPLIPILEVINICVPPREVTNPLKSVKRMKESLDET	242
DB	210	ENFKKLRFDPFLDPFLSTVFPPLIPILEVINICVPPREVTNPLKSVKRMKESLDET	269
QY	243	OKHRVDFLOIMDSQSKETESHKALSDLEVAQSIIFIPAGYETTSVLSFTMYELATH	302
DB	270	OKHRVDFLOIMDSQSKETESHKALSDLEVAQSIIFIPAGYETTSVLSFTMYELATH	329
QY	303	PVQQLQGEIDAVLNKAPPTVDTVLQMEYLDMMVNNETLRPLIARLERVCKKQVEIN	362

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Db 330 PDVQQLQGEIDAVLPNKAPPTVDYLQMEYLDVNVNETHLRLPIAMRLERVCCKDVEIN 389
|||
Qy 363 GMFIPKGVVVMIPSYALHRDPKWTBPEKFLPERFSKKNKNDIDPIYTPFGSGPRNCIG 422
|||
Db 390 GMFIPKGVVVMIPSYALHRDPKWTBPEKFLPERFSKKNKNDIDPIYTPFGSGPRNCIG 449
|||
Qy 423 MRPALNMKALIRVLQNSFKPKCKETOIPLKLSIGLLQPEKPVVLKVESRDGTIVSGA 481
|||
Db 450 MRPALNMKALIRVLQNSFKPKCKETOIPLKLSIGLLQPEKPVVLKVESRDGTIVSGA 508
|||
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RESULT 2

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US-09-949-016-8562
; Sequence 8562 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8562
; LENGTH: 508
; TYPE: PR1
; ORGANISM: Human
US-09-949-016-8562
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Query Match 98.4%; Score 2501; DB 4; Length 508;

Best Local Similarity 100.0%; Pred. No. 3.4e-244; Indels 0; Gaps 0;

Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 3 YGTHSHGLPKKLGIPGPTPLPFLGNILSYHKFCMFDECHCKYKVGWGYDGOQPVLA1 62
|||
Db 30 YGTHSHGLPKKLGIPGPTPLPFLGNILSYHKFCMFDECHCKYKVGWGYDGOQPVLA1 89
|||
Qy 63 TDPDMIKTVLYKCYSVFTNRRPFGVGFPMKSAISIAEDBEWKRLSLSPFTSGKLKE 122
|||
Db 90 TDPDMIKTVLYKCYSVFTNRRPFGVGFPMKSAISIAEDBEWKRLSLSPFTSGKLKE 149
|||
Qy 123 MVEPIIAQYGDVLYRNLRREAETGKPVTLKDVFGAYSMDVITSTSGVINIDSLNPPDPEV 182
|||
Db 150 MVEPIIAQYGDVLYRNLRREAETGKPVTLKDVFGAYSMDVITSTSGVINIDSLNPPDPEV 209
|||
Qy 183 ENTKKLRFDFLPDFLSTVFPPLIPLEVNLCVFPREVTNPLKSKYKRMKESRLDET 242
|||
Db 210 ENTKKLRFDFLPDFLSTVFPPLIPLEVNLCVFPREVTNPLKSKYKRMKESRLDET 269
|||
Qy 243 QKRRVDFLOLMDISQNSKTESHKALSDLEVAQSIIFPAGYETTSSVLSFIMYELATH 302
|||
Db 270 QKRRVDFLOLMDISQNSKTESHKALSDLEVAQSIIFPAGYETTSSVLSFIMYELATH 329
|||
Qy 303 PDVQQLQGEIDAVLPNKAPPTVDYLQMEYLDVNVNETHLRLPIAMRLERVCCKDVEIN 362
|||
Db 330 PDVQQLQGEIDAVLPNKAPPTVDYLQMEYLDVNVNETHLRLPIAMRLERVCCKDVEIN 389
|||
Qy 363 GMFIPKGVVVMIPSYALHRDPKWTBPEKFLPERFSKKNKNDIDPIYTPFGSGPRNCIG 422
|||
Db 390 GMFIPKGVVVMIPSYALHRDPKWTBPEKFLPERFSKKNKNDIDPIYTPFGSGPRNCIG 449
|||
Qy 423 MRPALNMKALIRVLQNSFKPKCKETOIPLKLSIGLLQPEKPVVLKVESRDGTIVSGA 481
|||
Db 450 MRPALNMKALIRVLQNSFKPKCKETOIPLKLSIGLLQPEKPVVLKVESRDGTIVSGA 508
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RESULT 3

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US-09-144-367-2
; Sequence 2, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
; APPLICANT: Licher, Jay
; APPLICANT: Guido, Marco
; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
; FILE REFERENCE: SEQ-12P
; CURRENT APPLICATION NUMBER: US/09/144,367
; CURRENT FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/058,612
; PRIOR FILING DATE: 1997-09-10
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 503
; TYPE: PR1
; ORGANISM: H. sapiens
US-09-144-367-2
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Query Match 98.1%; Score 2494; DB 4; Length 503;

Best Local Similarity 99.8%; Pred. No. 1.7e-243; Indels 1; Gaps 0;

Matches 478; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

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Qy 3 YGTHSHGLPKKLGIPGPTPLPFLGNILSYHKFCMFDECHCKYKVGWGYDGOQPVLA1 62
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Db 25 YGTHSHGLPKKLGIPGPTPLPFLGNILSYHKFCMFDECHCKYKVGWGYDGOQPVLA1 84
|||
Qy 63 TDPDMIKTVLYKCYSVFTNRRPFGVGFPMKSAISIAEDBEWKRLSLSPFTSGKLKE 122
|||
Db 85 TDPDMIKTVLYKCYSVFTNRRPFGVGFPMKSAISIAEDBEWKRLSLSPFTSGKLKE 144
|||
Qy 123 MVEPIIAQYGDVLYRNLRREAETGKPVTLKDVFGAYSMDVITSTSGVINIDSLNPPDPEV 182
|||
Db 145 MVEPIIAQYGDVLYRNLRREAETGKPVTLKDVFGAYSMDVITSTSGVINIDSLNPPDPEV 204
|||
Qy 183 ENTKKLRFDFLPDFLSTVFPPLIPLEVNLCVFPREVTNPLKSKYKRMKESRLDET 242
|||
Db 205 ENTKKLRFDFLPDFLSTVFPPLIPLEVNLCVFPREVTNPLKSKYKRMKESRLDET 264
|||
Qy 243 QKRRVDFLOLMDISQNSKTESHKALSDLEVAQSIIFPAGYETTSSVLSFIMYELATH 302
|||
Db 265 QKRRVDFLOLMDISQNSKTESHKALSDLEVAQSIIFPAGYETTSSVLSFIMYELATH 324
|||
Qy 303 PDVQQLQGEIDAVLPNKAPPTVDYLQMEYLDVNVNETHLRLPIAMRLERVCCKDVEIN 362
|||
Db 325 PDVQQLQGEIDAVLPNKAPPTVDYLQMEYLDVNVNETHLRLPIAMRLERVCCKDVEIN 384
|||
Qy 363 GMFIPKGVVVMIPSYALHRDPKWTBPEKFLPERFSKKNKNDIDPIYTPFGSGPRNCIG 422
|||
Db 385 GMFIPKGVVVMIPSYALHRDPKWTBPEKFLPERFSKKNKNDIDPIYTPFGSGPRNCIG 444
|||
Qy 423 MRPALNMKALIRVLQNSFKPKCKETOIPLKLSIGLLQPEKPVVLKVESRDGTIVSGA 481
|||
Db 445 MRPALNMKALIRVLQNSFKPKCKETOIPLKLSIGLLQPEKPVVLKVESRDGTIVSGA 503
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RESULT 4

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US-09-949-016-8561
; Sequence 8561 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
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#
# PRIOR FILING DATE: 2000-10-03
# PRIOR APPLICATION NUMBER: 60/231,498
# PRIOR FILING DATE: 2000-09-08
# NUMBER OF SEQ ID NOS: 207012
# SOFTWARE: FASTSEQ for Windows Version 4.0
# SEQ ID NO 8561
# LENGTH: 508
# TYPE: PR1
# ORGANISM: Human
US-03-949-016-8561

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Query Match	87.8%	Score 2233;	DB 4;	Length 508;
Best Local Similarity	88.7%	Pred. No. 4.6e-217;		
Matches 425; Conservative	27;	Mismatches 27;	Indels 0;	Gaps 0;

Qy	3	YGHSHGIGFEKGLGIGPPTPLPFLNGIISLYHNGCFMFDECHCKGKGVGFDDQOPLVAI	62
Db	30	YGTHTHGLFEKGLGIGPPTPLPFLNGIISLFRKGYWTFDECHCKRKRWGIGIDCQPMIAI	89
Qy	63	TDPMIKITLVKECYSVFTRNRRPPGVPFGMKSAISIADEEWMKRLSILSPFTSGKKE	122
Db	90	TDPMIKITLVKECYSVFTRNRRPPGVPFGMKSAISIADEEWMKRLSILSPFTSGKKE	149
Qy	123	MVPIIAQGVLYVNLIRREAEATGKPYTLKQVFGVSMVIVITSGVNIIDSLNNQDPEV	182
Db	150	MVPIIAQGVLYVNLIRREAEATGKPYTLKQVFGVSMVIVITSGVNIIDSLNNQDPEV	209
Qy	183	ENTKGLLRFDPLDBPFLSITVFPPLPIPLEVANI CVFPEAYTFPRKSVKSKSRLEDT	242
Db	210	ENTKGLLRFPDLDPFLVSTIKVFPPLPIPLEALNITVFPKRVISPLTKSVKQIKGRLKET	269
Qy	243	QKHVDPLOLMIIDSONSKETESHKALSLELVAQSIITIPAGYETTSVSLFIMELATH	302
Db	270	QKHVDPLOLMIIDSONSKDSETHKALSLELVAQSIITIPAGYETTSVSLFIITELATH	329
Qy	303	PDVQOKLOEIDAVLPNKAPPTYDTVLOMEYLDVMVNTLTLPLFIAMLEBVCCKDVAIN	362
Db	330	PDVQOKLOEIDVLPNKAPPTYDTVLOEYLDVMVNTLTLPLFIAMLEBVCCKDVAIN	389
Qy	363	GMFIPKGVVMI PSYALHRDPRKYTEPEKFLPERFSKKNKONIDPIYITPFGSGHRNCIG	422
Db	390	GMFIPKGVVMI PSYVLHHDPRKYTEPEKFLPERFSKKNKONIDPIYITPFGSGHRNCIG	449
Qy	423	MRFLNMKKALIVLONFSFKPCKEIQIPIKLRSGLLOEBKBPVULKVESRDGIVSQA	481
Db	450	MRFLVNMKKALIVLONFSFKPCKEIQIPIKLRSGLLTLKEKPLVLAESRDEIVSQA	508

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RESULT 5
US-09-949-016-5992
; Sequence 5992, Application US/09949016
; Patent No. 681233
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH TYPE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5992
; LENGTH: 502
; TYPE: PR1
; ORGANISM: Human
; US-09-949-016-5992

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Query Match	84.3%;	Score 2142.5;	DB 4;	Length 502;
Best Local Similarity	84.1%;	Pred. No. 6.5e-208;		
Matches 402;	Conservative 37;	Mismatches 38;	Indels 1;	Gaps 1;

Qy	3	YGHSHLPPKKGIGPGTPIPLGONIIISYHKFGCMFMECHKKYGKMGFIDGQPLVAI	62
Dp	25	YGRTHHLFRKRGIGPGTPIPLGONVSTYQGLMKPTBCKYKKGXMGCTYEGGLPLVAI	84
Qy	63	TDPDMIKTVLVKBCYSVFTNRPRPGVPGFMKSAISIADEEMKRLNSLPTTSGKJKE	122
Dp	85	TDPPVIRTVLVKECYSVFTNRRSISGPGFMKSAISIADEEMKRLNSLPTTSGKJKE	144
Qy	123	MVPIIAYGVIVRNILREAEATGKPVTLKOVFGYSMDVTSTSGNINISLNNPDOPFV	182
Dp	145	MFPIIAOYGVIVRNILREAEATGKPVTLKOVFGYSMDVTSTSGNINISLNNPDOPFV	204
Qy	183	ENTKKLLRPDLDPFPLSTVFPPLPILEVLNLCVPREVTNPLRSVGRMKSRLDET	242
Dp	205	ESTKKFLKFGDLDPFLSTILFPPLVTFELANVSLPKOTINFLSIVRMKKSRLNDK	264
Qy	243	QKQRVDFLQIMIDONSKEFHSHKSLDLELVAOSIIFRAGETTSVSLFMYELATH	302
Dp	265	QKRLDLFLQIMIDONSKEFHSHKSLDLELVAOSIIFRAGETTSVSLFMYELATH	324
Qy	303	PDVOQKIQOEIDAVLPKAPPTDYVQMEYLDLVNVVETRLPLIARLBRVCKGVN	362
Dp	325	PDVOQKIQOEIDAVLPKAPPTDYVQMEYLDLVNVVETRLPLIARLBRVCKGVN	384
Qy	363	GMFIPKGVVMIPIYSALHRDPKWTBEBKFLPERFSKKNKNDIDPIYTFPGSGPRNCIG	422
Dp	385	GVFIPIKGSVMVIFPYALHDPKWTBEBEBRPERFSCK-KOSIDPIYTFPGSGPRNCIG	443
Qy	423	MRELNMKALIRVLONSFSFKCKEQIDPLKIDQGLQPEKPIYLVKVSRODTLSG	480
Dp	444	MRELNMKALIRVLONSFSFKCKEQIDPLKIDQGLQPEKPIYLVKVSRODTLSG	501

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RESULT 6
US-09-949-016-7091
: Sequence 7091, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL001307
: CURRENT APPLICATION NUMBER: US/09/949, 016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,438
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 7091
: LENGTH: 507
: TYPE: PRT
: ORGANISM: Human
: US-09-949-016-7091

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Query Match	84.3%	Score 2142.5;	DB 4;	Length 507;
Best Local Similarity	84.1%	Pred. No. 6.6e-208		
Matches	402;	Conservative	37;	Mismatches 38; Indels 1; Gaps 1;

QY	3	YGHSHGLPKKGLPGPTPLPGTGNLSYKGCMSWDMEDCKKYGKYGSGPDQOPLAI	62
DB	30	YGRIRHLEFKRLGLPGPTPLPGTGNLSYKGCMSWDMEDCKKYGKYGSGPDQOPLAI	89
QY	63	TDDPMIKTVLWKECYSVFNRRPFGVGFPMKSAISIAEDEMKRLNLSIPTSGLKE	122
DB	90	TDDDVIRTVLWKECYSVFNRRRLGPGVFMKSAISIAEDEMKRLNLSIPTSGLKE	149

QY	3	YGHSHGCLPKKGLIIPETPLRPLGNIISLTHKSGCMEDMCKKKYKVMYERDDQOPLAI	62
Db	30	YGRHHEFLKRLGILPGFTPLRLGAVLSLTKQGLMKRDTDECYKKYKGMVIGDGLPLVAI	89
QY	63	TDDPMIKTVLVEKCYSVFTNRRPFGVGFPMKSAISIAEDEMRLNLSLPTSGLKE	122
QY	90	TDDDVIRTVLVEKCYSVFTNRRSLGPGFMKSAISIAEDEMRLNLSLPTSGLKE	149

Oy	123	WVPIIAQGDVAVRNLRRRAETGKPYTLKDVGAGYEMDVYITSSPFGVINDLSLNNPDDPV	182
Db	150	MFPIIAQGDVAVRNLRRRAEKGKPYTLKDVFGASMDVYITGSPFGVINDLSLNNPDDPV	209
Oy	183	ENTKKLLEFDLPDFELSTIVPEFLPILEAVNI CVFPREVNTFLKSKYKRMKESRLBEDT	242
Db	210	ESTKKFLKGFDPDFELSTILFPFLPPVEALNVSPFPDITNIFLKSVMRMKKSRLNDK	269
Oy	243	OKHRDPIQIMDMSONSKETESHKALSDLEVAOSIIFPAGYETSSVLSFLMYELATH	302
Db	270	QKHRDPIQIMDMSONSKETESHKALSDLELAOSIIFPAGYETSSVLSFLMYELATH	329
Oy	303	PDVQOKLOEIDAVLPNKAPPTYDVTVLQMEYIDMVVNETLRLPLIAMLRLERYCKKQVEIN	362
Db	330	PDVQOKLOEIDAVLPNKAPPTYDVAVQMEYIDMVVNETLRLPLFPVAILRLERTCKKQVEIN	389
Oy	363	GMFPIKGVVVMPSVALHBDPKYMTPEKFLPERFSKKONKNDIPYIYPPGSGPRNCG	422
Db	390	GVFIPIKGSVMVPTVALHBDPKYMTPEEERFBRERFSK-KDSIDPIYIYPPGSGPRNCG	448
Oy	423	MRPALNMKALIRVLQNSFPKCKETQIPLKSLGGLIQEKPVVLYKVESRDGVSG	480
Db	449	MRPALNMKALIRVLQNSFPKCKETQIPLKSLDITGGLQEPKPIVLKXDSRGTISG	506

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RESULT 7
US-09-583-447A-2
; Sequence 2, Application US/09583447A
; Patent No. 6645745
; GENERAL INFORMATION:
; APPLICANT: WOJNOWSKI, Leszek
; APPLICANT: GELINER, Klaus
; APPLICANT: EISELT, Regina
; TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
; FILE REFERENCE: 310115.401
; CURRENT APPLICATION NUMBER: US/09/583,447A
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-583-447A-2

```

Query Match	77.0%;	Score 1957;	DB 4;	Length 503;
Best Local Similarity	76.2%;	Pred. No. 3.9e-189;		
Matches 364;	Conservative 51;	Mismatches 63;	Indels 0;	Gaps 0;

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0Y 5 YGTHSHGLPKLGI9RPTPLPLGLNLTLSHKRCMPDMCHKKYKGVMP9DQOVLAI 62
Db 25 YGTHSHKLFKKLGI9RPTPLPLFGTLLPLFRGLMNDRCRCNEXKYGMMGJYEBQO0PULVI 84
0Y 63 TDPDMIKTVLVECSVFTNRRPFGVGFEMKSLISIA2BEMKRLSLSPFTSGLKE 122
Db 85 MDPMIKTVLVECSVFTNOMPLGMMGLKSLSLABEBEMKRIITLSPATSVKFE 144
0Y 123 MVIPIAQYDVLVRNIRREAETGKPYTLKDFGAYSMDYITSTSPGVNIDSLNPDPPV 182
Db 145 MVIPIISQGDMLVRSIRGAENSKSLNLDKDFGAYTMDYITGTLFGVINDSLNPD0PFL 204
0Y 183 ENTUKLRLRDPDFLDFPLSTLTVPPFLPILEVLNLCVPPREVTNFKKSVKRMESRL0PT 242
Db 205 KMKMLKTLKDFLDFPLFLSLPPLVPEBALNIGLPPDVHFLKNSIRKMSRRLKOK 264
0Y 243 QKGRVDFLQMLTDSQSKSTESHKSLSDLELVAQSIITFAGYETTSVSLPIMYELATH 302
Db 265 QKGRVDFPQOMLDSQSKSTKSHKSLSDLELVAQSIITIFAAVDTTSTLPIMYELATH 324
0Y 303 PDVQKLOEBEIDAVLPENKAPPTVDFVLQWEMVNETLRLPIAMRLERVKQK0VEIN 362

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Db 325 PDVQGLQEBIDAVLPNKAPVITYDALLQMEYIDMWVNETLAPFVVSRYVRVCKDQIDLEIN 364

QY 363 GMEIPKGVVMMIPSYALHEDPKYTWBPEKFLPERFSKKNNKIDPIYTPPGSGPACIG 422

Db 385 GVLPFGGLMWMEIYALHHDPKYTWBPEKFCERSKKNKSIDLYRIPFGADPNRIG 444

QY 423 MRPALMMKLALRYLQNFSPKCKETOIPLKSLSGGLLOEKEPVLLKVESRDGTSG 480

Db 445 MRPALNINIKLAVRALQNFSPKCKETOIPLKDLNLPLOEKEIVLKVHLRDIITSG 502

RESULT 8
 US-08-457-274A-25
 : Sequence 25 Application US/08457274A
 : Patent No. 5734086
 : GENERAL INFORMATION:
 : APPLICANT: Scott, Jeffrey G.
 : APPLICANT: Tomita, Takashi
 : TITLE OF INVENTION: Cytochrome P4501pr Gene and Its Uses
 : NUMBER OF SEQUENCES: 29
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: Nixon, Hargrave, Devans & Doyle
 : STREET: P.O. Box 1051, Clinton Square
 : CITY: Rochester
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 14603
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/457,274A

```

1 CLASSIFICATION: 800
2
3 ATTORNEY/AGENT INFORMATION:
4
5 NAME: Goldman, Michael L.
6
7 REGISTRATION NUMBER: 30,727
8
9 REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)
10
11 TELECOMMUNICATION INFORMATION:
12
13 TELEPHONE: 716-263-1304
14
15 TELEFAX: 716-263-1600
16
17 INFORMATION FOR SEQ ID NO: 25:
18
19 SEQUENCE CHARACTERISTICS:
20
21 LENGTH: 504 amino acids
22
23 TYPE: amino acid
24
25 STRANDEDNESS: single
26
27 TOPOLOGY: linear
28
29 MOLECULE TYPE: protein
30
31 HYPOTHEICAL: NO
32
33 ANTI-SENSE: NO
34
35 ORIGINAL SOURCE:
36
37 ORGANISM: Rat
38
39 STRAIN:
40
41 DEVELOPMENTAL STAGE: Adult
42
43 POSITION IN GENOME:
44
45 CHROMOSOME/SEGMENT:
46
47 US-08-457-274A-25

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	Query Match	76.6%	Score 1946.5;	DB 1;	Length 504;	
	Best Local Similarity	74.0%;	Pred. No. 4.5e-188;			
	Matches	355;	Conservative	62;	Mismatches	62;
					Indels	1;
					Gaps	1
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OY	3 YGTHSHGLFKKLGIGTPPTPLPPLNLISLYHKFCFMFDMECHKKYGRKWGFNYGOQPVLA I	62				
	: : : : : : : : : : : : : : : : : : : : : : : : :					
Db	25 FGTRHGHGFKKQGIIPGPRLPFPGFVNLNYMGLWMTDVECHKKKGKIGLFGQGMPLEFAI	84				
OY	63 TDPDWIKVLVKECVSVFTNNRPPGGVFQMFSALSIADDEWKRLRSLSLPFTSGKLAE	122				
	: : : : : : : : : : : : : : : : : : : : : : : : :					
Db	85 TDTEHTKNLVAKECFSVFETNRRDDFPVGIMGKAUSAADDEMKRRFRALLSPFTSGRLKE	144				
OY	123 MWPIIAQGDVLVRNLIRREAREATGKRVTLKDVGAYSMVDITSTSPGVNDISLNPNODPEV	182				

Db 145 MFPIIEQGDILVAKYKQAEATGKPVTKKVFAGAYSDVITSTSGVNVDSLNNPKDPFV 204
Qy 183 ENTAKLIRPFLDPFSLITVPPLIPLILEVANI CVPREVTNFKRSVKRMSRLDET 242
Db 205 EKTQGLRPFPPFDLPFLSVLPFLTPPIEYEMLANI CMPEKOSIEFFKFFVYMKETRLDSV 264
Qy 243 QKRHVDFLOLMIDSON-SKETESHKALSDELVAOSIIFPAGETTSVLSFTMYELAT 301
Db 265 QKRHVDFLOLMNNHNSKDSKESHSTALSDEMTILOSIIIFPAGYEPSTSTLSFVLSHSLAT 324
Qy 302 HPDVQOKLQOEIIDLAVLNKAPPTDYVLQMEYLDMMVNETLRPLPIAMLERVCKDVEI 361
Db 325 HPDQOKLQOEIIDLALPNKAPPTDYVMEMEYLDMMVNETLRPLPIGNRLERVCKDVEI 384
Qy 362 NGAFIPGVVVMISYALHRDPKWTBDEKFLPERFSKKNKNDIPYIYPPGSGPNCI 421
Db 385 NGVFMFGSVVMTPSVALHDPQHMPEBEPERFSKKNKSIDPYVYLPPFGGPNNCI 444
Qy 422 GMRPALNMMLALIRVLONSFKPKCKETOIPLKISLGILQPEKPVVLAKESRDGTVSGA 481
Db 445 GMRPALNMMLALIRVLONSFKPKCKETOIPLKISLGILQPTKPIILKVPREDIITGS 504

RESULT 9

US-09-583-447A-4
Sequence 4, Application US/09583447A
Patent No. 6645745
GENERAL INFORMATION:
APPLICANT: WOJNOMSKI, Leszek
APPLICANT: GELMAN, Klaus
APPLICANT: EISELT, Regina
TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
FILE REFERENCE: 31015.401
CURRENT APPLICATION NUMBER: US/09/583, 447A
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 504
TYPE: PRT
ORGANISM: Homo sapiens
US-09-583-447A-4

Query Match 76.6%; Score 1946.5; DB 4; Length 504;
Best Local Similarity 76.0%; Pred. No. 4.5e-188;
Matches 364; Conservative 51; Mismatches 63; Indels 1; Gaps 1;

Qy 3 YGTHSHGLFKKLGIPGPTLPPLIGNILSYHKGFQCMPEMECHKYGGKVMGFYDGOQVLA 62
Db 25 YGTHSHGLFKKLGIPGPTLPPLIGTILFYLRGLNWFRECKEYGGKVMGFYDGOQVLA 84
Qy 63 TDPDMIKTIVLVKESVFTNRPRPGVGFPMKSAISIADEBEMKRLSLSPFTSGKLKE 122
Db 85 MDDDMIKTIVLVKESVFTNQMPGPMGFLKSALSPADEBEMKRIKILSLPFTSVKFE 144
Qy 123 MVDIIAQYDVLVRNLRRAEATGKPVTLKDVFGAYSMDVITSTSGVNI DSI LNNPODPFV 182
Db 145 MVDIIAQYDVLVRNLRRAEATGKPVTLKDVFGAYSMDVITSTSGVNI DSI LNNPODPFV 204
Qy 183 ENTAKLIRPFLDPFSLITVPPLIPLILEVANI CVPREVTNFKRSVKRMSRLDET 242
Db 205 EKTQGLRPFPPFDLPFLSVLPFLTPPIEYEMLANI CMPEKOSIEFFKFFVYMKETRLDSV 264
Qy 243 QKRHVDFLOLMIDSON-SKETESHKALSDELVAOSIIFPAGETTSVLSFTMYELAT 302
Db 265 QKRHVDFLOLMIDSON-SKETESHKALSDELVAOSIIFPAGETTSVLSFTMYELAT 324
Qy 302 HPDVQOKLQOEIIDLAVLNKAPPTDYVLQMEYLDMMVNETLRPLPIAMLERVCKDVEI 362
Db 325 HPDQOKLQOEIIDLALPNKAPPTDYVMEMEYLDMMVNETLRPLPIGNRLERVCKDVEI 384

Qy 363 GMRIPKGVVVMIPSYALHRDPKWTBDEKFLPE-RSEKKNKNDIPYIYPPGSGPNCI 421
Db 385 GMRIPKGVVVMIPSYALHRDPKWTBDEKFLPERFSKKNKNDIPYIYPPGSGPNCI 444
Qy 422 GMRPALNMMLALIRVLONSFKPKCKETOIPLKISLGILQPEKPVVLAKESRDGTVSG 480
Db 445 GMRPALNMMLALIRVLONSFKPKCKETOIPLKISLGILQPTKPIILKVPREDIITGS 503

RESULT 10

PCT-US95-05758-25
Sequence 25, Application PC/TUS9505758
GENERAL INFORMATION:
APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: Cytochrome P4501pr Gene and Its
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: P.O. Box 1051, Clinton Square
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05758
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/241 (D-1519)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1600
TELEFAX: 716-263-1304
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Rat
STRAIN: Unknown
DEVELOPMENTAL STAGE: Adult
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Unknown
PCT-US95-05758-25

Query Match 76.6%; Score 1946.5; DB 5; Length 504;
Best Local Similarity 74.0%; Pred. No. 4.5e-188;
Matches 355; Conservative 62; Mismatches 62; Indels 1; Gaps 1;

Qy 3 YGTHSHGLFKKLGIPGPTLPPLIGNILSYHKGFQCMPEMECHKYGGKVMGFYDGOQVLA 62
Db 25 YGTHSHGLFKKLGIPGPTLPPLIGTILFYLRGLNWFRECKEYGGKVMGFYDGOQVLA 84
Qy 63 TDPDMIKTIVLVKESVFTNRPRPGVGFPMKSAISIADEBEMKRLSLSPFTSGKLKE 122
Db 85 TDPDMIKTIVLVKESVFTNRPRPGVGFPMKSAISIADEBEMKRIKILSLPFTSVKFE 144
Qy 123 MVDIIAQYDVLVRNLRRAEATGKPVTLKDVFGAYSMDVITSTSGVNI DSI LNNPODPFV 182
Db 145 MVDIIAQYDVLVRNLRRAEATGKPVTKKVFAGAYSDVITSTSGVNVDSLNNPKDPFV 204

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11162
LENGTH: 554
TYPE: PRT
ORGANISM: Human
US-09-949-016-11162

Query Match 33.1%; Score 840.5; DB 4; Length 554;
Best Local Similarity 35.9%; Pred. No. 4.6e-76;
Matches 183; Conservative 100; Mismatches 182; Indels 45; Gaps 10;

QY YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDECHKKYKGVWGFYDGOQPVLA1 62
DB YSTASFSLEKLGRLHPRSPFIGNLTFRQGFMSQMLKLYGLPLGLYGRMFLVI 111
QY TDDPMIKTVLVKCYSVFTNRPRPGVGFMSAIS1--AEDEWKRSLSLPTFTSGKL 120
DB SEPMIKQVLY-ENMSFTNFMASG-LEFKSVADSVLRLDKRMBEYVAGALMSAFSPKEL 169
QY 121 KEMPIIAQGVLYVNLREAEATGKPYTLKOVFGAYSMDVITSTSGVNIDSLNPPDP 180
DB 170 NEMVPLISQACDLILAHKRYAESGDADIORCYCNYTDDVAVAFGTPTDVSQAPEDP 229
QY 181 FVEVTKLRLRFPDLPFLSTVPP-FLPILEVNLICVPR---EVTNLRKSVKRMK 235
DB 230 FVKKCKRFFECIRPIIVLVLSFSPSIVPLARIL-----DNKRDLENGFNKLIRNVI 284
QY 236 ESR-LEDTPKHVRVDFLOLMIDONS-----KETESH----- 265
DB 285 ALRQQAEEERRRDFLOVNLARBSASPMGVODPIVADVSSGCKENPBRQHPSPMA 344
QY 266 KALSDLELVASITFIPIFGYTTSSVLSFIYELATHPDVOQKIOEIDAVLPKAPPTY 325
DB 345 RPLTVDEIVGQAFIFLAGYEIINTLSFATYLATNPDCQCKLRLREVDFEKKHMAPEF 404
QY 326 DTVLQ-MEYLDVMVNETLRFPIMRLERVCXKQVEINGMFIPKGVVMMISVALHDPK 384
DB 405 CSLEEGFLYLDVLAETLRMPAPRFTREAAQCEVVGORI PAGAVLEMAVGLHDPPE 464
QY 385 YMTPEPEKFLPERFESKKNKONIDPIYITPFSGPRNCIGPAPALNMKLALIRVLONFSFK 444
DB 465 HMPSEPFENPERFAPABARQOHRPFTYLPFGAGPRSCGVRGLLEVLTLTLHVLHKKRFQ 524
QY 445 PCKETQIPLKSLGGLLOPEKPVVLKVESR 474
DB 525 ACPEVQVPLQESKALGPKNGVYIKVISR 554

RESULT 14
US-09-583-447A-8
Sequence 8, Application US/09583447A
Patent No. 6645745
GENERAL INFORMATION:
APPLICANT: MOUNOMSKI, Legezek
APPLICANT: GERLINER, Klaus
APPLICANT: EISELT, Regina
TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
FILE REFERENCE: 310115.401
CURRENT APPLICATION NUMBER: US/09/583,447A

CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 8
LENGTH: 250
TYPE: PRT
ORGANISM: Homo sapiens
US-09-583-447A-8

Query Match 31.5%; Score 802; DB 4; Length 250;
Best Local Similarity 73.9%; Pred. No. 1e-72;
Matches 147; Conservative 23; Mismatches 29; Indels 0; Gaps 0;

QY YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDECHKKYKGVWGFYDGOQPVLA1 62
DB YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDECHKKYKGVWGFYDGOQPVLA1 84
QY TDDPMIKTVLVKCYSVFTNRPRPGVGFMSAIS1AEDEWKRSLSLPTFTSGKLKE 122
DB MDPMIKTVLVKCYSVFTNRPRPGVGFMSAIS1AEDEWKRSLSLPTFTSGKLKE 144
QY 123 MVIPIAQGVLYVNLREAEATGKPYTLKOVFGAYSMDVITSTSGVNIDSLNPPDPFV 182
DB 145 MVIPIAQGVLYVNLREAEATGKPYTLKOVFGAYSMDVITSTSGVNIDSLNPPDPFV 204
QY 183 ENTCKLRLRFPDLPFLSTI 201
DB 205 KMKKQLKLDLPFLFLLI 223

RESULT 15
US-09-270-767-46468
Sequence 46468, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 46468
LENGTH: 529
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-46468

Query Match 28.4%; Score 721.5; DB 4; Length 529;
Best Local Similarity 33.9%; Pred. No. 4.8e-64;
Matches 172; Conservative 111; Mismatches 181; Indels 43; Gaps 16;

QY YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDECHKKYKGVWGFYDGOQPVLA1 57
DB 32 WASANNDFFKORGLAIEKPYLVFGNMAQMLRKAMFDIVCDLYTKGSKKPGIETFORQ 91
QY 58 PVLAITDDPMIKTVLVKCYSVFTNR-----PFGPVGFMSAIS1AEDEWKRSL 107
DB 92 PLMVVRDPLIKQITIKD-FDHFIRNRNVPAATSDDDPHMSMLFGSSLSRMDARWKM 150
QY 108 RSLSPFTSGKLKEMVPIIAQGVLYVNLREAEATGKPYTLKOVFGAYSMDVITST 165
DB 151 RSTLSPAFSGSKOROMFQOLANOVAKAVDCLKODSDRVOENBMDKDYCTRFNTDVAST 210
QY 166 SFGVNIDSLNPPDPFENTCKLRLRFPDLPFLSTVPPFLPILEVNLICVPRPVN 225
DB 211 AFGQVNSPDRNTPIYQMKKLTFTTFLDS--MKMTLFPALGLKILKAVELPDKSTQ 268
QY 226 -FLRKSVMKESRLSDYQK---RVDFLOLMIDONSKETESHKA-----LSDELVAQ 276
DB 269 YFVRLVLDAMKY-----RQEHNIVRPMINMLMEARGIQTETKSAVAVESGDRDVAQ 323
QY 277 SIIFPIAGYTTSSVLSFIYELATHPDVOQKIOEIDAV---LPNKAPPTYTVLQMEY 333

[illegible]

Search completed: July 8, 2005, 14:14:55
Job time : 32 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2005, 14:10:22 ; Search time 175 Seconds

(without alignments)
1419.191 Million cell updates/sec

Title: US-10-690-991-2

Perfect score: 2542

Sequence: 1 MARGTSHGLFKKLGIRGPT.....PVLAKVSRDQTVSGANHHH 485

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2501	98.4	503	2	086SK3
2	2494	98.1	503	1	CP34_HUMAN
3	2449.5	96.4	503	1	CP33_HUMAN
4	2372	93.3	503	1	CP38_MACFA
5	2372	93.3	503	2	Q6VP01
6	2366	93.1	503	2	Q6PSM4
7	2283	89.8	503	1	CP31_CALJA
8	2233	87.8	503	1	CP37_HUMAN
9	2215	87.0	503	2	Q9H281
10	2212	87.0	430	2	Q7Z448
11	2142.5	84.3	502	1	CP35_HUMAN
12	2112	83.1	503	2	Q6GUD3
13	2077	81.7	503	1	CP3C_CANFA
14	2025	79.7	503	2	Q8H2K1
15	2000	78.7	503	1	CP39_RAT
16	1997	78.2	503	1	CP30_SHEEP
17	1989	78.6	501	1	CP36_RABIT
18	1983	78.0	503	1	CP3T_PIG
19	1979	77.9	503	2	Q97689
20	1961	77.1	503	1	CP3D_MOUSE
21	1957	77.0	503	1	CP343_HUMAN
22	1952	76.8	503	2	Q95LJ5
23	1946.5	76.6	504	1	CP31_RAT
24	1935.5	76.1	504	1	CP3B_MOUSE
25	1929	75.9	503	2	Q76N65
26	1918.5	75.5	504	1	CP32_RAT
27	1906.5	75.0	504	1	CP341_MOUSE
28	1904.5	74.9	502	2	Q6LEQ2
29	1902.5	74.8	502	2	Q6LEQ2
30	1885	74.2	497	2	Q8CJF2
31	1885	74.2	507	1	CP3S_BOVIN

32	1884	74.1	503	1	CP3E_CAVPO	Q64417	cavia porce
33	1878.5	73.9	504	1	CP3G_MOUSE	Q64481	mus musculus
34	1877	73.8	503	1	CP3F_MOUSE	Q09158	mus musculus
35	1876	73.8	503	2	Q9QXK4	Q9QXK4	mus musculus
36	1857	73.1	503	1	CP3F_CAVPO	Q64406	cavia porce
37	1849.5	72.8	504	2	Q9EQM4	Q64409	mus musculus
38	1846	72.6	503	1	CP3H_CAVPO	Q64409	cavia porce
39	1835	72.2	501	1	CP3V_MESAU	Q70537	mesocricetu
40	1802	70.9	497	1	CP3I_RAT	Q64581	rattus norv
41	1788	70.3	503	1	CP3A_MESAU	Q64148	mesocricetu
42	1696	66.7	353	2	Q86SK2	Q86SK2	homo sapien
43	1596	62.8	508	2	Q9PU44	Q9PU44	gallus galli
44	1560.5	61.4	504	2	Q6PAL1	Q6PAL1	xenopus lae
45	1550	61.0	496	1	CP30_PUNHE	Q9PVE8	fundulus he

ALIGNMENTS

RESULT 1

ID	086SK3	PRELIMINARY;	PRT;	503 AA.
AC	086SK3;			
DT	01-JUN-2003 (TrEMBLrel. 24, Created)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	Cytochrome P450.			
GN	Name=CYP3A43/CYP3A4;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RP	TISSUE=Liver;			
RA	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: Belongs to the cytochrome P450 family.			
DR	EMBL; AJ563375; CAD91343.1; -.			
DR	HSSP; P14779; LJPZ.			
DR	GO; GO:0005624; C:membrane fraction; TAS.			
DR	GO; GO:0004497; F:monooxygenase activity; IDA.			
DR	GO; GO:0006005; P:steroid hormone 6-beta-hydroxylase activity; IDA.			
DR	InterPro; IPR001128; Cytochrome_P450.			
DR	InterPro; IPR002401; EP4501.			
DR	InterPro; IPR008072; EP450_CYP3A.			
DR	Pfam; PF00067; P450; 1.			
DR	PRINTS; PR00463; EP4501.			
DR	PRINTS; PR01689; EP4501CYP3A.			
DR	PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.			
KW	Heme; Monooxygenase; Oxidoreductase.			
SQ	SEQUENCE 503 AA; 57394 MW; 4141P95B28B34A6E CRC64;			
Query Match	98.4%; Score 2501; DB 2; Length 503			
Best Local Similarity	100.0%; Pred. No. 3.8e-174;			
Matches	479; Conservative 0; Mismatches 0; Indels			
QY	3 YGHSHGLPKKLGIRGPTLPPIGNLSTYHKGCMQDMCKKKYK			
DB	25 YGHSHGLPKKLGIRGPTLPPIGNLSTYHKGCMQDMCKKKYK			
QY	63 TDPDMIKTVLVKCYGVFTNRRPFGVGVKMSAISTADEMY			
DB	85 TDPDMIKTVLVKCYGVFTNRRPFGVGVKMSAISTADEMY			

QY 123 MPEIIAOGDVLVRNLRREAETGKPVTLKOVFGAYSMDVITSTSPGVDITSLNNPODPV 182
DB 145 MPEIIAOGDVLVRNLRREAETGKPVTLKOVFGAYSMDVITSTSPGVDITSLNNPODPV 204
QY 183 ENTKKLLRPDLDPFPLSLITVPPLIPILEVNIICVFPREVNTLKRKYVRKMSKSLDEPT 242
DB 205 ENTKKLLRPDLDPFPLSLITVPPLIPILEVNIICVFPREVNTLKRKYVRKMSKSLDEPT 264
QY 243 OKRRVDFLOLMIDSONSKETESHKALSDLELVAGSIIIFIPAGYETTSVLSFTMYELATH 302
DB 265 OKRRVDFLOLMIDSONSKETESHKALSDLELVAGSIIIFIPAGYETTSVLSFTMYELATH 324
QY 303 PDVQOKLOEETIDAVLPNKAPPTVDYLOMEYLDMMVNETLRPLIMRLERVKKKVEIN 362
DB 325 PDVQOKLOEETIDAVLPNKAPPTVDYLOMEYLDMMVNETLRPLIMRLERVKKKVEIN 384
QY 363 GMFIPKGVVMIPIPSYALHDPKYTEPEKELPERFSKKNKNDIPYIYTPFGSGPRNCIG 422
DB 385 GMFIPKGVVMIPIPSYALHDPKYTEPEKELPERFSKKNKNDIPYIYTPFGSGPRNCIG 444
QY 423 MRPALMMKALIRVTONSFCKCKETOIPLKLSIGGLLOPEKPVVLKYESRDGTVSGA 481
DB 445 MRPALMMKALIRVTONSFCKCKETOIPLKLSIGGLLOPEKPVVLKYESRDGTVSGA 503

RESULT 2

CP34_HUMAN STANDARD; PRT; 502 AA.
ID P08684; Q16757; Q9UK50;
AC 01-JAN-1988 (Rel. 06, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cytochrome P450 3A4 (EC 1.14.13.67) (Quinine 3-monooxygenase)
DE (CYP11A4) (Nifedipine oxidase) (NF-25) (P450-PCNI).
GN Name=CYP3A4;
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88195781; PubMed=3267210;
RA Gonzalez F.J., Schmid B.J., Umeno M., McBride O.W., Hardwick J.P.,
RA Meyer U.A., Gelboin H.V., Idle J.R.;
RT "Human P450PCNI: sequence, chromosome localization, and direct
RT evidence through cDNA expression that P450PCNI is nifedipine
RT oxidase.";
RL DNA 7:79-86(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87041402; PubMed=3464943;
RA Beuane P.H., Umbenhauer D.R., Bork R.W., Lloyd R.S., Genglerich F.P.;
RT "Isolation and sequence determination of a cDNA clone related to human
RT cytochrome P-450 nifedipine oxidase.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8064-8068(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89108438; PubMed=2563251;
RA Spurr N.K., Gough A.C., Stevensen K., Wolf C.R.;
RT "The human cytochrome P450 CYP3 locus: assignment to chromosome 7q22-
RT qter.";
RL Hum. Genet. 81:171-174(1989).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89093163; PubMed=2463251;
RA Bork R.W., Muto T., Beuane P.H., Srivastava P.K., Lloyd R.S.,
RA Genglerich F.P.;
RT "Characterization of mRNA species related to human liver cytochrome P-
RT 450 nifedipine oxidase and the regulation of catalytic activity.";
RL J. Biol. Chem. 264:910-919(1989).
RN [5]

RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=99256082; PubMed=10322772;
RA Chen Q., Wu J., Yu Y.;
RT "Establishment of transgenic cell line CHL-3A4 and its metabolic
RT activation.";
RL Zhonghua Yu Fang Yi Xue Za Zhi 32:281-284(1998).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=21163842; PubMed=11266076;
RA Gellner K., Eiselt R., Huster E., Arnold H., Koch I., Haberl M.,
RA Deglmann C.J., Burk O., Buntefuss D., Escher S., Bishop C.,
RA Koeps H.-G., Brinkmann U., Klenk H.-P., Kleine K., Meyer U.A.,
RA Wojnowski L.;
RT "Genomic organization of the human CYP3A locus: identification of a
RT new, inducible CYP3A gene.";
RL Pharmacogenetics 11:111-121(2001).
RN [7]
RP SEQUENCE FROM N.A., AND VARIANTS VAL-117 AND ARG-217.
RX MEDLINE=21098888; PubMed=1181494;
RA Heien K.-P., Lin Y.-Y., Cheng C.-L., Lai M.-L., Lin M.-S.,
RA Sies J.-P., Huang J.-D.;
RT "Novel mutations of CYP3A4 in Chinese.";
RL Drug Metab. Dispos. 29:268-273(2001).
RN [8]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Zhuge J., Qian Y., Xie H., Yu Y.;
RT "Sequence of a new human cytochrome P450-3A4 cDNA.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [9]
RP CHARACTERIZATION.
RX MEDLINE=97243737; PubMed=9088578;
RA Zhang H., Coville P.F., Walker R.J., Miners J.O., Birrell D.J.,
RA Wanyimoluk S.;
RT "Evidence for involvement of human CYP3A in the 3-hydroxylation of
RT quinine.";
RL Br. J. Clin. Pharmacol. 43:245-252(1997).
RN [10]
RP CHARACTERIZATION.
RX MEDLINE=9812830; PubMed=9456308;
RA Zhao X.J., Kawashiro T., Ishizaki T.;
RT "Mutual inhibition between quinine and ecoposide by human liver
RT microsomes. Evidence for cytochrome P4503A4 involvement in their major
RT metabolic pathways.";
RL Drug Metab. Dispos. 26:188-191(1998).
RN [11]
RP VARIANTS PRO-221 AND THR-444.
RX MEDLINE=20132287; PubMed=1068853; DOI=10.1067/mcp.2000.104391;
RA Sata F., Sapone A., Eliscando G., Stocker P., Miller V.P., Zheng W.,
RA Raulo H., Crepiti C.L., Gonzalez P.J.;
RT "CYP3A4 allelic variants with amino acid substitutions in exons 7 and
RT 12: evidence for an allelic variant with altered catalytic activity.";
RL Clin. Pharmacol. Ther. 67:48-56(2000).
RN [12]
RP VARIANTS GLN-161; SER-188; PRO-292; THR-444 AND SER-466, AND
RP CHARACTERIZATION OF THE VARIANTS.
RX MEDLINE=21571796; PubMed=11714865;
RA Dai D., Tang J., Rose R., Hodgson E., Bienstock R.J.,
RA Mohentzler H.W., Goldstein J.A.;
RT "Identification of variants of CYP3A4 and characterization of their
RT abilities to metabolize testosterone and chlorpyrifos.";
RL J. Pharmacol. Exp. Ther. 299:825-831(2001).
RN [13]
RP VARIANTS ASP-55; GLN-129; ILE-169; HIS-173; MET-362; PHE-372 AND
RP LEU-415.
RX MEDLINE=21364010; PubMed=11470997;
RA Eiselt R., Domanski T.L., Zibat A., Mueller R., Prescan-Siedel E.,
RA Huster E., Zanger U.M., Brockmoller J., Klenk H.-P., Meyer U.A.,
RA Khan K.K., He Y.-A., Halpert J.R., Wojnowski L.;
RT "Identification and functional characterization of eight CYP3A4
RT protein variants.";
RL Pharmacogenetics 11:447-458(2001).

RN [14]
 RE VARIANTS PRO-14: GIN-161; HIS-173; SER-184 AND PHR-372.
 RX MEDLINE=21864884; PubMed=11875366;
 RA Lamba J.K., Lin Y.S., Thummel K., Daly A., Watkins P.B., Strom S.,
 RT Zhang J., Schuetz E.G.;
 RA "Common allelic variants of cytochrome P450A4 and their prevalence in
 RT different populations";
 RL Pharmacogenetics 12:121-132(2002).
 CC -1- FUNCTION: Cytochromes P450 are a group of heme-thiolate
 CC monooxygenases. In liver microsomes, this enzyme is involved in an
 CC NADPH-dependent electron transport pathway. It performs a variety
 CC of oxidation reactions (e.g. caffeine 8-oxidation, omeprazole
 CC sulfoxidation, midazolam 1'-hydroxylation and midazolam 4-
 CC hydroxylation) of structurally unrelated compounds, including
 CC steroids, fatty acids, and xenobiotics. The enzyme also
 CC hydroxylates etoposide.
 CC -1- CATALYTIC ACTIVITY: Quinine + NADPH + O(2) = 3-hydroxyquinine +
 CC NADP(+) + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: Expressed in prostate and liver.
 CC -1- INDUCTION: P450 can be induced to high levels in liver and other
 CC tissues by various foreign compounds, including drugs, pesticides,
 CC and carcinogens.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 CC -1- DATABASE: NAME=Cytochrome P450 Allele Nomenclature Committee;
 CC NOTE=CYP3A4 alleles;
 CC WWW="http://www.imm.ki.se/CYPalleles/cyp3a4.htm".
 CC -----
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 CC -----
 DR EMBL: M18907; AAA35745.1; -;
 DR EMBL: M14096; AAA35744.1; -;
 DR EMBL: X12387; CAA30944.1; -;
 DR EMBL: J04449; AAA35747.1; -;
 DR EMBL: AF182273; AAF13598.1; -;
 DR EMBL: AF280107; AAG32290.1; -;
 DR EMBL: AF209389; AAF21034.1; -;
 DR PIR: A29815; A29815.
 DR HSSP: P14779; IUPZ.
 DR Genew: HGNC:2637; CYP3A4.
 DR MIM: 124010; -;
 DR GO: GO:0005624; C:membrane fraction; ISS.
 DR GO: GO:0004497; F:monooxygenase activity; ISS.
 DR GO: GO:0019825; F:oxygen binding; TAS.
 DR GO: GO:0006629; P:lipid metabolism; TAS.
 DR GO: GO:0006805; P:xenobiotic metabolism; ISS.
 DR InterPro: IPR001128; Cytochrome P450.
 DR InterPro: IPR008072; EP450 CYP3A.
 DR InterPro: IPR002401; EP450I.
 DR Pfam: PF00067; P450; 1.
 DR PRINTS: PR00463; EP450I.
 DR PRINTS: PR01689; EP450IICYP3A.
 DR PRINTS: PR00385; P450.
 DR PROSITE: PS00086; CYTOCHROME P450; 1.
 KM Electron transport: Endoplasmic reticulum; Heme; Membrane; Microsome;
 KM Monooxygenase; NADP; Oxidoreductase; Polymorphism.
 FT INIT_MET 0
 FT METAL 441 441
 FT VARIANT 14 14
 FT VARIANT 55 55
 FT VARIANT 117 117
 FT VARIANT 129 129
 FT VARIANT 161 161
 FT VARIANT 161 161
 R -> I (in allele CYP3A4*9).
 R -> H (in allele CYP3A4*10).
 R -> S (in allele CYP3A4*16).
 R -> Q (in allele CYP3A4*8).
 R -> Q (in allele CYP3A4*15).

FT VARIANT 169 169
 FT VARIANT 173 173
 FT VARIANT 184 184
 FT VARIANT 188 188
 FT VARIANT 188 188
 Query Match
 Best Local Similarity 98.1%; Score 2494; DB 1; Length 502;
 Matches 478; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 YGTHSHGLFKKGI PGPTPLPGLNLSYHKGFCMPDMECHKYKGYMGFYDGOQPYLA1 62
 DB 24 YGTHSHGLFKKGI PGPTPLPGLNLSYHKGFCMPDMECHKYKGYMGFYDGOQPYLA1 83
 QY 63 TDSDMTKTVLYKCYSVFTNRPRPGVGFPMKSA1S1AEDEMKRLSLSPFTSGKLE 122
 DB 84 TDSDMTKTVLYKCYSVFTNRPRPGVGFPMKSA1S1AEDEMKRLSLSPFTSGKLE 143
 QY 123 MPEIIAQYGVLYVRLNREAEKGPVTLKDFAGYSMDVITSTFGVNIIDSLNPPDPFV 182
 DB 144 MPEIIAQYGVLYVRLNREAEKGPVTLKDFAGYSMDVITSTFGVNIIDSLNPPDPFV 203
 QY 183 ENTFKLIRPFDLPPLSTVPPPLIPLEVINI CYPREVNTFLRKSVMKESRLSDT 242
 DB 204 ENTFKLIRPFDLPPLSTVPPPLIPLEVINI CYPREVNTFLRKSVMKESRLSDT 263
 QY 243 QKRHVDLOIMDSQSKESHKALSDLELVNOSITTFRAGETTSVSFTMYELATH 302
 DB 264 QKRHVDLOIMDSQSKESHKALSDLELVNOSITTFRAGETTSVSFTMYELATH 323
 QY 303 PDVQOQLQSEIDAVLPNKAAPTDTVLOMSYLDVNVNETHLPPIAMRLERVKQVEIN 362
 DB 324 PDVQOQLQSEIDAVLPNKAAPTDTVLOMSYLDVNVNETHLPPIAMRLERVKQVEIN 383
 QY 363 GMFIPKGVVMIPISYALHRDPKWTPEKFLPERFSKKNKNDIPYIYTPFGSGPNCIG 422
 DB 384 GMFIPKGVVMIPISYALHRDPKWTPEKFLPERFSKKNKNDIPYIYTPFGSGPNCIG 443
 QY 423 MRPALNMKALRLVONSPFKCKETQYPLKSLIGLQPKRPVYLKVESRGTVSGA 481
 DB 444 MRPALNMKALRLVONSPFKCKETQYPLKSLIGLQPKRPVYLKVESRGTVSGA 502
 RESULT 3
 CP33_HUMAN STANDARD; PRT; 503 AA.
 AC P05184;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cytochrome P450 3A3 (EC 1.14.14.1) (CYP11A3) (HLP).
 GN Name=CYP3A3;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=86259780; PubMed=346094;
 RA Molowa D.T., Schuetz E.G., Wright S.A., Watkins P.B., Kremers P.,
 RA Mendez-Picon G., Parker G.A., Guzelian P.S.;
 RT "Complete cDNA sequence of a cytochrome P-450 inducible by
 RT glucocorticoids in human liver";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5311-5315(1986).
 RN [2]
 RP SEQUENCE OF 1-20.
 RC TISSUE=Liver;
 RX MEDLINE=85298342; PubMed=3898085;

RA Watkins P.B., Wrighton S.A., Maurel P., Schuetz E.G., Mendez-Picon G.,
 RA Parker G.A., Guzelian P.S.;
 RT "Identification of an inducible form of cytochrome P-450 in human
 RT liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6310-6314 (1985).
 CC -1- FUNCTION: Cytochromes P450 are a group of heme-thiolate
 CC monooxygenases. In liver microsomes, this enzyme is involved in an
 CC NADPH-dependent electron transport pathway. It oxidizes a variety
 CC of structurally unrelated compounds, including steroids, fatty
 CC acids, and xenobiotics.
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
 CC oxidized flavoprotein + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
 CC -1- INDUCTION: By glucocorticoids.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.

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 DR EMBL: D00003; BAA00001.1; -;
 DR EMBL: M13785; AAA35742.1; -;
 DR PIR: A29410; A29410.
 DR HSSP: P14779; 1JFZ.
 DR GeneW: HGNC:2636; CYP3A3.
 DR GO: GO:0005624; C:membrane fraction; ISS.
 DR GO: GO:0005792; C:microsome; TAS.
 DR GO: GO:0004497; F:monooxygenase activity; ISS.
 DR GO: GO:0019825; F:oxygen binding; TAS.
 DR GO: GO:0006805; P:xenobiotic metabolism; ISS.
 DR InterPro: IPR001128; Cytochrome_P450.
 DR InterPro: IPR008072; EP450_CYP3A.
 DR InterPro: IPR002401; EP450_I.
 DR Pfam: PF00067; P450; 1.
 DR PRINTS: PR00463; EP450I.
 DR PRINTS: PR00385; P450.
 DR PRINTS: PR01689; EP450IICYP3A.
 DR PROSITE: PS00086; CYTOCHROME_P450; 1.
 DR Direct protein sequencing; Electron transport; Endoplasmic reticulum;
 KM Heme; Membrane; Microsome; Monooxygenase; Oxidoreductase.
 FT INIT MET 0 0
 FT METC 442 442 Iron (heme axial ligand) (By similarity).
 SQ SEQUENCE 503 AA; 57428 MW; 9885D1F729658FC0 CRC64;

 Query Match 96.4%; Score 2449.5; DB 1; Length 503;
 Best Local Similarity 97.9%; Pred. No. 2.2e-170;
 Matches 470; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

 QY 3 YGHSIGLFRKGLIGPTPLPFLGNLSTYKGFCEMDMECHKYKGYMGFYDGOQVLA 62
 DB 24 YGHSIGLFRKGLIGPTPLPFLGNLSTYKGFCEMDMECHKYKGYMGFYDGOQVLA 83
 QY 63 TDPMDKTVLVKESYVFTRNRPFGVGFEMKSAISTAEDBEMRLSLSPFTSKLXE 122
 DB 84 TDPMDKTVLVKESYVFTRNRPFGVGFEMKSAISTAEDBEMRLSLSPFTSKLXE 143
 QY 123 MVEPIAOGDVLVRLNRREAEATGKPYTLKDFGAGMDVITSTFGVNIDSLNPPDPFY 182
 DB 144 MVEPIAOGDVLVRLNRREAEATGKPYTLKDFGAGMDVITSTFGVNIDSLNPPDPFY 203
 QY 183 ENTTKLIRDFLDLPPFLSTVPPFLIPLEVLNIQVPRPVNLFKSKYKMKESLDEPT 242
 DB 204 ENTTKLIRDFLDLPPFLSTVPPFLIPLEVLNIQVPRPVNLFKSKYKMKESLDEPT 263
 QY 243 OKHRVDFLOLMIDS-ONSKESTESHKALSDLEIVAOSIIFPACYETTSVLSIWEALF 301
 DB 264 OKHRVDFLOLMIDS-ONSKESTESHKALSDLEIVAOSIIFPACYETTSVLSIWEALF 323
 QY 302 HPDVQOKLOEIDAVALPNKAPPTVDTVLQMEYLDVMVNETLRLFLPAMLERVCKDVEI 361

DB 324 HPDVQOKLOEIDAVALPNKAPPTVDTVLQMEYLDVMVNETLRLFLPAMLERVCKDVEI 383
 QY 362 NGMFIPKGVVMI PSYALHRDPKYTEPEKFLPERPSKKXNDIDPIYTPGSGPRNCI 421
 DB 384 NGMFIPKGVVMI PSYALHRDPKYTEPEKFLPERPSKKXNDIDPIYTPGSGPRNCI 443
 QY 422 GMRFLMNMKALITVLQWESFPCKEIQIPIKLSIGGLQPEKVVYLVKESRDGVSGA 481
 DB 444 GMRFLMNMKALITVLQWESFPCKEIQIPIKLSIGGLQPEKVVYLVKESRDGVSGA 503

 RESULT 4
 CP38 MACFA STANDARD; PRT; 503 AA.
 ID CP38 MACFA PRT; 503 AA.
 AC P33268; P25231;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cytochrome P450 3A8 (EC 1.14.14.1) (CYP11A8) (P450-MGNF2) (P-450-MK2).
 GN Name=CYP3A8;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OC NCBI_Taxid=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RC MEDLINE=93129612; PubMed=1282830; DOI=10.1016/0167-4776(92)90113-E;
 RA Komori M., Kikuchi O., Sakuma T., Funaki J., Kitada M., Kametaki T.;
 RT "Molecular cloning of monkey liver cytochrome P-450 cDNAs: similarity
 RL of the primary sequences to human cytochromes P-450.";
 RL Biochim. Biophys. Acta 1171:141-146 (1992).
 RN [2]
 RP SEQUENCE OF 1-22.
 RC TISSUE=Liver;
 RC MEDLINE=89287352; PubMed=2500151; DOI=10.1016/0167-4838(89)90107-6;
 RA Ohta K., Kitada M., Hashizume T., Komori M., Ohi H., Kametaki T.;
 RT "Purification of cytochrome P-450 from polychlorinated biphenyl-
 RT treated crab-eating monkeys: high homology to a form of human
 RL cytochrome P-450.";
 RL Biochim. Biophys. Acta 996:142-145 (1989).
 CC -1- FUNCTION: Catalyzes nifedipine and nifedipine oxidations.
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
 CC oxidized flavoprotein + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
 CC -1- INDUCTION: By polychlorinated biphenyl (PCB).
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.

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 DR EMBL: S53047; AAB24952.1; -;
 DR PIR: S28168; S28168.
 DR HSSP: P14779; 1JFZ.
 DR GO: GO:0005624; C:membrane fraction; ISS.
 DR GO: GO:0004497; F:monooxygenase activity; ISS.
 DR GO: GO:0006805; P:xenobiotic metabolism; ISS.
 DR InterPro: IPR001128; Cytochrome_P450.
 DR InterPro: IPR008072; EP450_CYP3A.
 DR InterPro: IPR002401; EP450_I.
 DR Pfam: PF00067; P450; 1.
 DR PRINTS: PR00463; EP450I.
 DR PRINTS: PR01689; EP450IICYP3A.
 DR PRINTS: PR00385; P450.
 DR PROSITE: PS00086; CYTOCHROME_P450; 1.

KW Direct protein sequencing; Electron transport; Endoplasmic reticulum;
KW Heme; Membrane; Mitochondria; Monooxygenase; Oxidoreductase.
FT METAL 442 442 Iron (heme axial ligand) (by similarity).
SQ SEQUENCE 503 AA; 57511 MW; D701B6FE83AC8BFB CRC64;
Query Match 93.3%; Score 2372; DB 1; Length 503;
Best Local Similarity 93.9%; Pred. No. 1e-164;
Matches 450; Conservative 18; Mismatches 11; Indels 0; Gaps 0;
QY 3 YGTHSHGLFKKLGIPGPTPLPPLGNILSYKGCMPDMECHKYKGYKMGFYDGOQPYLAI 62
DB 25 YGTHSHGLFKKLGIPGPTPLPPLGNILSYKGFMTDMECKYKGYKMGFYDGOQPYLAI 84
QY 63 TDDPMIKTVLVKCYSTFTNRPRPGPVGFPMKSAISIADEBEMKRLISLPTFTSGDLKE 122
DB 85 TDDPMIKTVLVKCYSTFTNRPRPGPVGFPMKSAISIADEBEMKRLISLPTFTSGDLKE 144
QY 123 MVEPIIAQGVLYVNLRRBAETGKPYTLKDVFGAYSMDVITSTSGVNIIDSLNPPDPFV 182
DB 145 MVEPIIAQGVLYVNLRRBAETGKPYTLKDVFGAYSMDVITSTSGVNIIDSLNPPDPFV 204
QY 183 ENTCKLARFPDLDPPLSLITVPPPLIPILEVNLICVPPREVNTNPLKSVKMKESRLDPT 242
DB 205 ENTCKLARFPDLDPPLSLITVPPPLIPILEVNLISIFPREVTSFLKSVKRIKESRLDPT 264
QY 243 QKHNVDFLOLMIDSQSKETESHKALSDLELVAOSIIFPAGYETTSVLSFTIMEYLATH 302
DB 265 QKHNVDFLOLMIDSQSKETESHKALSDLELVAOSIIFPAGYETTSVLSFTIMEYLATH 324
QY 303 PDVQOKLOEBIDAVLNKAPPTDYTLQMEYLDVNMVNETLRPIAMRLERVKCKOYEIN 362
DB 325 PDVQOKLOEBIDAVLNKAPPTDYTLQMEYLDVNMVNETLRPIAMRLERVKCKOYEIN 384
QY 363 GMFIPKGVVMIPISYALHRDPKWTBEPKFLPERFSKKNKNDIDPIYTFPGSGPRNCIG 422
DB 385 GFIPIKGVVMIPISYALHRDPKWTBEPKFLPERFSKKNKNDIDPIYTFPGSGPRNCIG 444
QY 423 MRPALNMKALIRVLONFSFKCKETOIPLKRLGSLQTEKPIVLKIESRDGTVSGA 481
DB 445 MRPALNMKALIRVLONFSFKCKETOIPLKRLGSLQTEKPIVLKIESRDGTVSGA 503

RESULT 5
Q6VP01 PRELIMINARY; PRT; 503 AA.
ID Q6VP01
AC Q6VP01;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome P450 3A64.
GN Name=CYP3A64;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Booth-Genthe C.L., Rushmore T.H.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL: AY34551; AAP94642.1; -
DR GO: GO:0004497; F:monooxygenase activity; IEA.
DR GO: GO:0016712; F:oxidoreductase activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR001128; Cytochrome_P450.
DR InterPro: IPR002401; BP4501.
DR InterPro: IPR008072; BP450_CYP3A.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00463; BP4501.
DR PRINTS: PR01689; BP4501CYP3A.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.
DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.

KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 503 AA; 57511 MW; D701B6FE83AC8BFB CRC64;
Query Match 93.3%; Score 2372; DB 2; Length 503;
Best Local Similarity 93.9%; Pred. No. 1e-164;
Matches 450; Conservative 18; Mismatches 11; Indels 0; Gaps 0;
QY 3 YGTHSHGLFKKLGIPGPTPLPPLGNILSYKGCMPDMECHKYKGYKMGFYDGOQPYLAI 62
DB 25 YGTHSHGLFKKLGIPGPTPLPPLGNILSYKGFMTDMECKYKGYKMGFYDGOQPYLAI 84
QY 63 TDDPMIKTVLVKCYSTFTNRPRPGPVGFPMKSAISIADEBEMKRLISLPTFTSGDLKE 122
DB 85 TDDPMIKTVLVKCYSTFTNRPRPGPVGFPMKSAISIADEBEMKRLISLPTFTSGDLKE 144
QY 123 MVEPIIAQGVLYVNLRRBAETGKPYTLKDVFGAYSMDVITSTSGVNIIDSLNPPDPFV 182
DB 145 MVEPIIAQGVLYVNLRRBAETGKPYTLKDVFGAYSMDVITSTSGVNIIDSLNPPDPFV 204
QY 183 ENTCKLARFPDLDPPLSLITVPPPLIPILEVNLICVPPREVNTNPLKSVKMKESRLDPT 242
DB 205 ENTCKLARFPDLDPPLSLITVPPPLIPILEVNLISIFPREVTSFLKSVKRIKESRLDPT 264
QY 243 QKHNVDFLOLMIDSQSKETESHKALSDLELVAOSIIFPAGYETTSVLSFTIMEYLATH 302
DB 265 QKHNVDFLOLMIDSQSKETESHKALSDLELVAOSIIFPAGYETTSVLSFTIMEYLATH 324
QY 303 PDVQOKLOEBIDAVLNKAPPTDYTLQMEYLDVNMVNETLRPIAMRLERVKCKOYEIN 362
DB 325 PDVQOKLOEBIDAVLNKAPPTDYTLQMEYLDVNMVNETLRPIAMRLERVKCKOYEIN 384
QY 363 GMFIPKGVVMIPISYALHRDPKWTBEPKFLPERFSKKNKNDIDPIYTFPGSGPRNCIG 422
DB 385 GFIPIKGVVMIPISYALHRDPKWTBEPKFLPERFSKKNKNDIDPIYTFPGSGPRNCIG 444
QY 423 MRPALNMKALIRVLONFSFKCKETOIPLKRLGSLQTEKPIVLKIESRDGTVSGA 481
DB 445 MRPALNMKALIRVLONFSFKCKETOIPLKRLGSLQTEKPIVLKIESRDGTVSGA 503

RESULT 6
Q6PSM4 PRELIMINARY; PRT; 503 AA.
ID Q6PSM4
AC Q6PSM4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome P450 3A64 variant 1.
GN Name=CYP3A64;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Booth-Genthe C.L., Rushmore T.H.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL: AY582531; AAS91645.1; -
DR GO: GO:0004497; F:monooxygenase activity; IEA.
DR GO: GO:0016712; F:oxidoreductase activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR001128; Cytochrome_P450.
DR InterPro: IPR002401; BP4501.
DR InterPro: IPR008072; BP450_CYP3A.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00463; BP4501.
DR PRINTS: PR01689; BP4501CYP3A.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 503 AA; 57526 MW; E5206E2DAD8BAE28 CRC64;

Query Match 93.1%; Score 2366; DB 2; Length 503;
 Best Local Similarity 93.7%; Pred. No. 2.7e-164;
 Matches 449; Conservative 18; Mismatches 12; Indels 0; Gaps 0;

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QY 3 YGTHSHGLFKKGLIGPPTPLPLGNILSYHKGCFMDECHKRYGKYGWYDGOQVLA1 62
DB 25 YGTHSHGLFKKGLIGPPTPLPLGNILSYHKGCFMDECHKRYGKYGWYDGOQVLA1 84
QY 63 TDPDMIKTVLVKCYSVFTNRPRPGVGMKSAISIAEBEKKRLRLSLSPFTSGKLKE 122
DB 85 TDENMKTIVLVKCYSVFTNRPRPGVGMKSAISIAEBEKKRLRLSLSPFTSGKLKE 144
QY 123 MVEPIIAQYGDVLRNLRRAEATGKPVTLKQVFGAYSMDVITSTSGVNIIDSLNNPDPPV 182
DB 145 MVEPIIAQYGDVLRNLRRAEATGKPVTLKQVFGAYSMDVITSTSGVNIIDSLNNPDPPV 204
QY 183 ENTCKLRLRFDLPDFPLSLITVPPFLIPILEVLNICVPREVTNPLKRSYKMKESRLBDT 242
DB 205 ENTCKLRLRFDLPDFPLSLITVPPFLIPILEVLNICVPREVTNPLKRSYKMKESRLBDT 264
QY 243 QKRRVDFLOLMIDSONSKETESHKALSDLEVAQSIIIFPAGYETTSVLSPITVELATH 302
DB 265 QKRRVDFLOLMIDSONSKETESHKALSDLEVAQSIIIFPAGYETTSVLSPITVELATH 324
QY 303 PDVQOKLOBEIDAVLPNKAPPTDYTVLQMEYLDVNVNETLRPLAMRLERCKKQVEIN 362
DB 325 PDVQOKLOBEIDAVLPNKAPPTDYTVLQMEYLDVNVNETLRPLAMRLERCKKQVEIN 384
QY 363 GMFIPKGVVMIPSYALHDPKYTEPEKFLPERFSKKNKNDIDYIYTPFGSGPRNCIG 422
DB 385 GFIIPKGVVMIPSYALHDPKYTEPEKFLPERFSKKNKNDIDYIYTPFGSGPRNCIG 444
QY 423 MRPALMMKALIRVLQNSFKCKETOIPLKRLIGGLQPEKPVVLKVESRGTVSGA 481
DB 445 MRPALMMKALIRVLQNSFKCKETOIPLKRLIGGLQPEKPVVLKVESRGTVSGA 503

RESULT 7
CP37_CALJA STANDARD; PRT; 503 AA.
AC 018993;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cytochrome P450 3A21 (EC 1.14.14.1) (CYP11A21) (P450 CM3A-10).
GN Name=CYP3A21;
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrich.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=97223367; PubMed=9056237; DOI=10.1006/abbi.1996.9852;
RA Igarashi T., Sakuma T., Isogai M., Nagata R., Kametaki T.;
RT "Marmoset liver cytochrome P450s: study for expression and molecular
RT cloning of their cDNAs."
RL Arch. Biochem. Biophys. 339:85-91(1997).
CC -1- FUNCTION: Cytochromes P450 are a group of heme-cholate
CC monooxygenases. In liver microsomes, this enzyme is involved in an
CC NADPH-dependent electron transport pathway. It oxidizes a variety
CC of structurally unrelated compounds, including steroids, fatty
CC acids, and xenobiotics.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- INDUCTION: P450 can be induced to high levels in liver and other
CC tissues by various foreign compounds, including drugs, pesticides,
CC and carcinogens.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
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DR EMBL; D31921; BAA2156.1; -.
DR HSSP; P14779; 1UPZ.
DR GO; GO:0005624; C:membrane fraction; ISS.
DR GO; GO:0004497; F:monooxygenase activity; ISS.
DR GO; GO:0006805; P:xenobiotic metabolism; ISS.
DR InterPro; IPR001128; Cytochrome P450.
DR InterPro; IPR008072; EP450 CYP3A.
DR InterPro; IPR002401; EP450T.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00463; EP450I.
DR PRINTS; PR01689; EP450IICYP3A.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME P450; 1.
KW Electron transport; Endoplasmic reticulum; Heme; Membrane; Microsome;
KW Monooxygenase; Oxidoreductase.
FT METAL 442
FT ION 442 Iron (heme axial ligand) (By similarity).
SQ SEQUENCE 503 AA; 57564 MW; 9BPD421D72C76D6A CRC64;

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Query Match 89.8%; Score 2283; DB 1; Length 503;
 Best Local Similarity 90.0%; Pred. No. 3.2e-158;
 Matches 421; Conservative 26; Mismatches 22; Indels 0; Gaps 0;

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QY 3 YGTHSHGLFKKGLIGPPTPLPLGNILSYHKGCFMDECHKRYGKYGWYDGOQVLA1 62
DB 25 YGTHSHGLFKKGLIGPPTPLPLGNILSYHKGCFMDECHKRYGKYGWYDGOQVLA1 84
QY 63 TDPDMIKTVLVKCYSVFTNRPRPGVGMKSAISIAEBEKKRLRLSLSPFTSGKLKE 122
DB 85 TDPNIIKTVLVKCYSVFTNRPRPGVGMKSAISIAEBEKKRLRLSLSPFTSGKLKE 144
QY 123 MVEPIIAQYGDVLRNLRRAEATGKPVTLKQVFGAYSMDVITSTSGVNIIDSLNNPDPPV 182
DB 145 MVEPIIAQYGDVLRNLRRAEATGKPVTLKQVFGAYSMDVITSTSGVNIIDSLNNPDPPV 204
QY 183 ENTCKLRLRFDLPDFPLSLITVPPFLIPILEVLNICVPREVTNPLKRSYKMKESRLBDT 242
DB 205 ENTCKLRLRFDLPDFPLSLITVPPFLIPILEVLNICVPREVTNPLKRSYKMKESRLBDT 264
QY 243 QKRRVDFLOLMIDSONSKETESHKALSDLEVAQSIIIFPAGYETTSVLSPITVELATH 302
DB 265 HKRRVDFLOLMIDSONSKETESHKALSDLEVAQSIIIFPAGYETTSVLSPITVELATH 324
QY 303 PDVQOKLOBEIDAVLPNKAPPTDYTVLQMEYLDVNVNETLRPLAMRLERCKKQVEIN 362
DB 325 PDVQOKLOBEIDAVLPNKAPPTDYTVLQMEYLDVNVNETLRPLAMRLERCKKQVEIN 384
QY 363 GMFIPKGVVMIPSYALHDPKYTEPEKFLPERFSKKNKNDIDYIYTPFGSGPRNCIG 422
DB 385 GFIIPKGVVMIPSYALHDPKYTEPEKFLPERFSKKNKNDIDYIYTPFGSGPRNCIG 444
QY 423 MRPALMMKALIRVLQNSFKCKETOIPLKRLIGGLQPEKPVVLKVESRGTVSGA 481
DB 445 MRPALMMKALIRVLQNSFKCKETOIPLKRLIGGLQPEKPVVLKVESRGTVSGA 503

RESULT 8
CP37_HUMAN STANDARD; PRT; 503 AA.
AC P24462;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cytochrome P450 3A7 (EC 1.14.14.1) (CYP11A7) (P450-HPLA).
GN Name=CYP3A7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal liver;
 RA MEDLINE=89255154; PubMed=2722762;
 RA Komori M., Nishio K., Ohl H., Kitada M., Kametaki T.;
 RT "Molecular cloning and sequence analysis of cDNA containing the entire
 RL coding region for human fetal liver cytochrome P-450".
 RL J. Biochem. 105:161-163(1989).
 [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=11263842; PubMed=11266076;
 RA Gellner K., Elselz R., Rustert B., Arnold H., Koch I., Habert M.,
 RA Deglmann C.J., Burk O., Buntelns D., Escher S., Bishop C.,
 RA Koese H.-G., Brinkmann U., Klenk H.-P., Kleine K., Meyer U.A.,
 RA Wojnowski L.;
 RT "Genomic organization of the human CYP3A locus: identification of a
 RL new, inducible CYP3A gene".
 RL Pharmacogenetics 11:111-121(2001).
 CC -1- FUNCTION: Cytochromes P450 are a group of heme-thiolate
 CC monooxygenases. In liver microsomes, this enzyme is involved in an
 CC NADPH-dependent electron transport pathway. It oxidises a variety
 CC of structurally unrelated compounds, including steroids, fatty
 CC acids, and xenobiotics.
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
 CC oxidized flavoprotein + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound, Endoplasmic reticulum.
 CC -1- INDUCTION: P450 can be induced to high levels in liver and other
 CC tissues by various foreign compounds, including drugs, pesticides,
 CC and carcinogens.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 CC -1- DATABASES: NAME=Cytochrome P450 Allele Nomenclature Committee;
 CC NOTE=CYP3A7 alleles;
 CC WWW="http://www.imm.ki.se/cypalleles/cyp3a7.htm".

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 CC or send an email to license@isb-sib.ch).

 DR EMBL, D00408; BAA00310.1; -;
 DR EMBL, AF280107; AAC32289.1; -;
 DR PIR, JX0062; JX0062.
 DR HSSP, P14779; JLPZ.
 DR Genew, HGNC:2640; CYP3A7.
 DR MIM, 605340; -;
 DR GO, GO:0005624; C:membrane fraction; ISS.
 DR GO, GO:0004497; F:monooxygenase activity; ISS.
 DR GO, GO:0019825; F:oxygen binding; TAS.
 DR GO, GO:0006805; P:xenobiotic metabolism; ISS.
 DR InterPro, IPR001128; Cytochrome_P450.
 DR InterPro, IPR008072; EP450_CYP3A.
 DR InterPro, IPR002401; EP450I.
 DR Pfam, PF00067; P450.1.
 DR PRINTS, PRO0463; EP450I.
 DR PRINTS, PRO1689; EP450ICYP3A.
 DR PRINTS, PRO0385; P450.
 DR PROSITE, PS00086; CYTOCHROME_P450.1.
 DR KEGG, K01101; Cytochrome P450; Heme; Membrane; Microsome;
 DR Monooxygenase; Oxidoreductase.
 FT METAL 442 442 Iron (heme axial ligand) (By similarity).
 SO SEQUENCE 503 AA; 57470 MW; 087CCEBDBAC14C CAC64;
 Query Match 87.8%; Score 2233; DB 1; Length 503;
 Best Local Similarity 88.7%; Pred. No. 1,4e-154;
 Matches 425; Conservative 27; Mismatches 27; Indels 0; Gaps 0;

[illegible]

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Db 25 YGRTTGLFCKKCIIPGPTLPFLGNALSPFKGYWTEDMECYKKRNVWGIDYDQGMAL 84
Qy 63 TDPDMIKTVLVKCYSVFTNRPPGPGFMKSAISIAEDEWRLASLSPTTSGLKE 122
Db 85 TDDMDIKTVLVKCYSVFTNRPPGPGFMKSAISIAEDEWRLASLSPTTSGLKE 144
Qy 123 MVEIINQGVVLVRNLRREAEKGKPVTLKDVFGAYSMDVITSTSFGVNIIDSLNPPDPV 182
Db 145 MVEIINQGVVLVRNLRREAEKGKPVTLKDVFGAYSMDVITSTSFGVNIIDSLNPPDPV 204
Qy 183 ENTKLLRPDLDPFLSLITVPEPLIPILEVNICVPEPREVITFLKSVKRMKESRLBDT 242
Db 205 ENTKLLRPDLDPFLSLITVPEPLIPILEVNICVPEPREVITFLKSVKRMKESRLBDT 264
Qy 243 QKRRVDFLOLMIDSONSKETESHKALSDELVAOSIIFIPAGYETTSVLSFTMTALAT 302
Db 265 QKRRVDFLOLMIDSONSKETESHKALSDELVAOSIIFIPAGYETTSVLSFTMTALAT 324
Qy 303 PDVQOKLOEIDAVLPNKAPPTVTLQMEYLDVNVNTETRLPIAMRLERVKDVEIN 362
Db 325 PDVQOKLOEIDAVLPNKAPPTVTLQMEYLDVNVNTETRLPIAMRLERVKDVEIN 384
Qy 363 GMFIPKGVVVMIPSYALHRDPKWTBEPKFLPERFSKKNKNDIPYIYTPFGSGPRNCIG 422
Db 385 GMFIPKGVVVMIPSYALHRDPKWTBEPKFLPERFSKKNKNDIPYIYTPFGSGPRNCIG 444
Qy 423 MRPALMMKALIRVLQNFSPKCKETQIPLKLSLGLLOPEKPVVLKESRGT 477
Db 445 MRPALMMKALIRVLQNFSPKCKETQIPLKLSLGLLOPEKPVVLKESRGT 499
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RESULT 10

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Q72448 PRELIMINARY; PRT; 430 AA.
ID Q72448
AC Q72448;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Cytochrome P450 (Fragment).
OS Name=CYP3A4;
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=21839017; PubMed=11726664; DOI=10.1074/jbc.M109175200;
RA Finta C., Zaphiropoulos P.G.;
RT "Intergenic mRNA molecules resulting from trans-splicing.";
RL J. Biol. Chem. 277:5882-5890(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Zaphiropoulos P.G.;
CC Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; A1563376; CAD91645.1; -.
DR HSSP; P14779; IUPZ.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450_1.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOW_1.
KW Heme; Monooxygenase; Oxidoreductase.
FT NON TER 1
SQ SEQUENCE 430 AA; 49137 MW; C232BF7E2571155C CRC64;
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Query Match 87.0%; Score 2212; DB 2; Length 430;
Best Local Similarity 100.0%; Pred. No. 3.9e-153;
Matches 430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 52 FYDGOQPVLAITDPDMIKTVLVKCYSVFTNRPPGPGFMKSAISIAEDEWRLASLS 111
Db 1 FYDGOQPVLAITDPDMIKTVLVKCYSVFTNRPPGPGFMKSAISIAEDEWRLASLS 60
Qy 112 SPTFTSGKLKENVPIIAQYGDVLVRNLRREAEKGKPVTLKDVFGAYSMDVITSTSFGVNI 171
Db 61 SPTFTSGKLKENVPIIAQYGDVLVRNLRREAEKGKPVTLKDVFGAYSMDVITSTSFGVNI 120
Qy 172 DSLNPPDPFVNTKLLRPDLDPFLSLITVPEPLIPILEVNICVPEPREVITFLKSV 231
Db 121 DSLNPPDPFVNTKLLRPDLDPFLSLITVPEPLIPILEVNICVPEPREVITFLKSV 180
Qy 232 KMKESRLBDTQKRRVDFLOLMIDSONSKETESHKALSDELVAOSIIFIPAGYETTSV 291
Db 181 KMKESRLBDTQKRRVDFLOLMIDSONSKETESHKALSDELVAOSIIFIPAGYETTSV 240
Qy 292 LSFIMYELATHDPVQOKLOEIDAVLPNKAPPTVTLQMEYLDVNVNTETRLPIAMRL 351
Db 241 LSFIMYELATHDPVQOKLOEIDAVLPNKAPPTVTLQMEYLDVNVNTETRLPIAMRL 300
Qy 352 ERVCKKDVINGMFIPKGVVVMIPSYALHRDPKWTBEPKFLPERFSKKNKNDIPYIYT 411
Db 301 ERVCKKDVINGMFIPKGVVVMIPSYALHRDPKWTBEPKFLPERFSKKNKNDIPYIYT 360
Qy 412 PGSGPRNCIGMRPALMMKALIRVLQNFSPKCKETQIPLKLSLGLLOPEKPVVLKV 471
Db 361 PGSGPRNCIGMRPALMMKALIRVLQNFSPKCKETQIPLKLSLGLLOPEKPVVLKV 420
Qy 472 ESRDGTVSGA 481
Db 421 ESRDGTVSGA 430
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RESULT 11

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CP35_HUMAN STANDARD; PRT; 502 AA.
ID CP35_HUMAN
AC P20815; Q9HBS6;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cytochrome P450 3A5 (EC 1.14.14.1) (CYP11A5) (P450-PCN3) (HLp2).
GN Name=CYP3A5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89278095; PubMed=2732228;
RA Aoyama T., Yamano S., Waxman D.J., Lapenson D.P., Meyer U.A.,
RA Fischer V., Tyndale R., Inaba T., Kalow W., Gelboin H.V.,
RA Gonzalez P.J.;
RT "Cytochrome P-450 hPCN3, a novel cytochrome P-450 IIIA gene product
RT that is differentially expressed in adult human liver. cDNA and
RT deduced amino acid sequence and distinct specificities of cDNA-
RT expressed hPCN1 and hPCN3 for the metabolism of steroid hormones and
RT cyclosporine."
RL J. Biol. Chem. 264:10388-10395(1989).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Colon;
RA Schuetz J.D., Molowa D.T., Guzelian P.S.;
RA PubMed=2802615;
RT "Characterization of a cDNA encoding a new member of the
RT glucocorticoid-responsive cytochromes P450 in human liver."
RL Arch. Biochem. Biophys. 274:355-365(1989).
RN [3]
RP SEQUENCE FROM N.A.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straussberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
Altehuil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkin R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Strepleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carinici P., Prange C.,
 RA Raha S.S., McQuellano N.A., Peters G.J., Adamson R.D., Mullaly S.J.,
 RA Bosak S.A., Logan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley D.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Vallalon D.K., Muzny K.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences." J.
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 1-106 FROM N.A.
 RX MEDLINE=21163842; PubMed=11266076;
 RA Gellner K., Eisele R., Hucbert E., Arnold H., Koch I., Haberl M.,
 RA Deglmann C.J., Burk O., Bunteluss D., Escher S., Bishop C.,
 RA Koebel H.-G., Birkmann U., Klenk H.-P., Kleine K., Meyer U.A.,
 RA Wojnowski L.;
 RT "Genomic organization of the human CYP3A locus: identification of a
 new, inducible CYP3A gene." J.
 RL Pharmacogenetics 11:111-121(2001).
 RN [5]
 RP SEQUENCE OF 1-24 FROM N.A.
 RX MEDLINE=96152836; PubMed=8569713;
 RA Schuetz J.D., Schuetz E.G., Thottassery J.V., Guzelian P.S., Strom S.,
 RT "Identification of a novel dexamethasone responsive enhancer in the
 human CYP3A5 gene and its activation in human and rat liver cells." J.
 RL Mol. Pharmacol. 49:63-72(1996).
 RN [6]
 RP VARIANT CYP3A5*2.
 RX MEDLINE=96192071; PubMed=8619878; DOI=10.1006/birc.1996.0618;
 RA Jounaidi Y., Hyattiles V., Gervot L., Maurel P.;
 RT "Detection of CYP3A5 allelic variant: a candidate for the polymorphic
 expression of the protein?" J.
 RL Biochem. Biophys. Res. Commun. 221:466-470(1996).
 CC -1- FUNCTION: Cytochromes P450 are a group of heme-thiolate
 monooxygenases. In liver microsomes, this enzyme is involved in an
 NADPH-dependent electron transport pathway. It oxidizes a variety
 of structurally unrelated compounds, including steroids, fatty
 acids, and xenobiotics.
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
 oxidized flavoprotein + H(2)O.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
 CC -1- INDUCTION: P450 can be induced to high levels in liver and other
 tissues by various foreign compounds, including drugs, pesticides,
 and carcinogens.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 CC -1- DATABASE: NMR-Cytochrome P450 Allele Nomenclature Committee;
 CC NOTE=CYP3A5 alleles;
 CC WWW=http://www.imm.ki.se/cypalleles/cyp3a5.htm".
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL: J04813; AAA02993.1; -
 DR EMBL: BC033862; AA033862.1; -
 DR EMBL: AF280107; AA032288.1; -
 DR EMBL: L35912; AA000083.1; -
 DR PIR: A34101; A34101.
 DR HSSP: P14779; IUPZ.
 DR Genew, HGNC:2638; CYP3A5.

DR H-INDB: HIX006899; -
 DR MIM: 603225; -
 DR GO: GO:0005624; C:membrane fraction, ISS.
 DR GO: GO:0005792; C:mitochondrion, TAS.
 DR GO: GO:0004497; F:monooxygenase activity, ISS.
 DR GO: GO:0019825; F:oxygen binding, TAS.
 DR GO: GO:0008202; P:steroid metabolism, TAS.
 DR GO: GO:0006805; P:xenobiotic metabolism, ISS.
 DR InterPro: IPR001128; Cytochrome_P450.
 DR InterPro: IPR008072; Cytochrome_P450.
 DR InterPro: IPR002401; BP4501.
 DR Pfam: PF00067; P450_1.
 DR PRINTS: PR00463; BP4501.
 DR PRINTS: PR01689; BP4501ICYP3A.
 DR PROSITE: PRO0385; P450.
 DR PROSITE: PS00086; CYTOCHROME_P450; 1.
 KW Electron transport; Endoplasmic reticulum; Heme; Membrane; Mitochondrion;
 KW Monooxygenase; Oxidoreductase; Polymorphism.
 FT METAL 441 441
 FT VARIANTS 398 398
 FT CONFLICT 305 305 /FTID=VAR_008365.
 FT CONFLICT 318 318 A -> P (in Ref. 2).
 FT CONFLICT 324 324 L -> F (in Ref. 2).
 FT CONFLICT 377 377 H -> D (in Ref. 2).
 FT CONFLICT 377 377 C -> G (in Ref. 2).
 SQ SEQUENCE 502 AA; 57108 MW; D5A230282633E717 CRC64;
 Query Match 84.3%; Score 2142.5; DB 1; Length 502;
 Best Local Similarity 84.1%; Pred. No. 5,8e-148;
 Matches 402; Conservative 37; Mismatches 38; Indels 1; Gaps 1;
 QY 3 YGTHSHGLFKKLDGPGPTPLPLGNLISYHKGFCMPDMECHKYKXWGYDQOPLYAI 62
 DB 25 YGTRHGLFRLGIPPTPLPLGNVLSYQGLMKPTECYKKGKGMKTYEQLPYLA 84
 QY 63 TDDPMIKTVLVKCYSTFNRRPFGVGFKSAISIAEDSEMRSLSPPTSGKLKE 122
 DB 85 TDDPVRITVAVKCYSTFNRRSLGPGVGFKSAISIAEDSEMRSLSPPTSGKLKE 144
 QY 123 MVDPIAQGVDAVRLNRRARETGKPVTLKDVFGAYSMDVITSTSPGVNIDSLNPPDPFV 182
 DB 145 MFDPIAQGVDAVRLNRRARETGKPVTLKDVFGAYSMDVITSTSPGVNIDSLNPPDPFV 204
 QY 183 ENTGKLRPFLDPFLSTVPPPLPILFVNLICVPPREVTNPLKRSVKRMSRLDET 242
 DB 205 ESTGKLRPFLDPFLSTVPPPLPILFVNLICVPPREVTNPLKRSVKRMSRLDET 264
 QY 243 QKRVDFLOLMIDSONSKETESHKALSDLELVNOSIIFPAGVETTSVLSFIMELATH 302
 DB 265 QKRVDFLOLMIDSONSKETESHKALSDLELVNOSIIFPAGVETTSVLSFIMELATH 324
 QY 303 PDVQOKLOEIDAVLNPKAPPTVTLVOMEVLDVNVNETHLPPIAMRLERVKDKVEIN 362
 DB 325 PDVQOKLOEIDAVLNPKAPPTVTLVOMEVLDVNVNETHLPPIAMRLERVKDKVEIN 384
 QY 363 GMFIPGVVMPISYALHRDPKTYTEDEKPLPERFSKKNIDPIYTPFGSGPNCIG 422
 DB 385 GMFIPGVVMPISYALHRDPKTYTEDEKPLPERFSKKNIDPIYTPFGSGPNCIG 443
 QY 423 MRPALMMKALIRVONSPKCKETQYPIKSLGLOPEKPVYLVKESRPGTUSG 480
 DB 444 MRPALMMKALIRVONSPKCKETQYPIKSLGLOPEKPVYLVKESRPGTUSG 501
 RESULT 12
 ID Q6GU03 PRELIMINARY; PRT; 503 AA.
 AC Q6GU03;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Cytochrome P450 CYP3A6.
 GN Name=CYP3A6;

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OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN (1)
RP SEQUENCE FROM N.A.
RA Carr B.A., Fang Y., Rushmore T.H.;
RU Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; A635466; AAT49270.1; -.
DR GO; GO:0004497; P:monooxygenase activity; IEA.
DR GO; GO:0016712; P:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP450I.
DR InterPro; IPR008072; EP450_CYP3A.
DR Pfam; PF00067; P450_1.
DR PRINTS; PR00463; EP450I.
DR PRINTS; PR01689; EP450IICYP3A.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 503 AA; 57382 MW; D0B8902ADDF3810 CRC64;

Query Match 83.1%; Score 2112; DB 2; Length 503;
Best Local Similarity 83.5%; Pred. No. 9.8e-146;
Matches 399; Conservative 34; Mismatches 45; Indels 0; Gaps 0;

QY 3 YGTHSHGLFKKLGIPGPTLPFLGNILSYHKFCMFDMCHKYKGVNGFYDGOQPVLA1 62
DB 25 YGTRSYGLFRRGQIPGPTLPFLGNILSYRQGLMKFPDTECYKKGKMMRTQDQLPVLRT 84
QY 63 TDDDMIKTVLVKCYSVFTNRRPFGVGFMSKSAISIAEDDEMRKLSLSPTTSGLKE 122
DB 85 TDEEMIKTVLVKCYSVFTNRRPFGVGLMSKSAISIAEDDEMRKLSLSPTTSGLKE 144
QY 123 MVEPIIAQYGDVAVRNLRAREATGKPVTLKDVFGAYSMDVITTSFGVNIIDSLNPPDPPV 182
DB 145 MPEPIIAQYGDVAVRNLRAREATGKPVTLKDVFGAYSMDVITTSFGVNIIDSLNPPDPPV 204
QY 183 ENTCKLRFDPDLPFLSTIVFPFLIPLEVLNIVCPREAVTNPLKSKYRMKESRLDET 242
DB 205 ESYVKKELKFDLPFLFLTLFPFLFPFALNVSILPPKDAINFLNKSVMMSKSLNDK 264
QY 243 QKRHVDFLOQIMDSQNSKETESHKALSDLELVAOSIIFIPAGYETTSVLSFIYBLATH 302
DB 265 QKRHVDFLOQIMDSQNSKETESHKALSDLELVAOSIIFIPAGYETTSVLSFIYBLATH 324
QY 303 PDVQOQKQOEIDAVLPKAPAPTYDVLQMEYLDVNVNVEITLRLPIAMRLERVCCKDVEIN 362
DB 325 PDVQOQKQOEIDAVLPKAPAPTYDVLQMEYLDVNVNVEITLRLPIAMRLERVCCKDVEIN 384
QY 363 GMFIPKGVVMIPTSYALHRDPKTYWTEBEKFLPERFSKKNKNDIDPIYITPFGSGPNNCTG 422
DB 385 GVFIIPKAMAVVITPYALHDPKTYWTEBEKFLPERFSKKNKNDIDPIYITPFGSGPNNCTG 444
QY 423 MRPALMMKALIRVLONSFSPCKEQTQIPLKSLGGLLOPEKPVVLKXSPRGCTVSG 480
DB 445 MRPALMMKALIRVLONSFSPCKEQTQIPLKSLGGLLOPEKPVVLKXSPRGCTVSG 502

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OC Mammalia; Eutheria; Carnivora; Flesipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=Beagle; TISSUE=Liver;
RX MEDLINE=91159488; PubMed=2001406; DOI=10.1016/0167-4781(91)90072-T;
RA Ciaccio P.J., Graves P.E., Bourque D.P., Glimsman-Gibson B.,
RA Halpert J.R.;
RT "cDNA and deduced amino acid sequences of a dog liver cytochrome P-450
of the IIA gene subfamily.";
RL Biochim. Biophys. Acta 1088:319-322(1991).
CC -1- FUNCTION: Cytochromes P450 are a group of heme-thiolate
monooxygenases. In liver microsomes, this enzyme is involved in an
NADPH-dependent electron transport pathway. It oxidizes a variety
of structurally unrelated compounds, including steroids, fatty
acids, and xenobiotics.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- INDUCTION: P450 can be induced to high levels in liver and other
tissues by various foreign compounds, including drugs, pesticides,
and carcinogens.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
-----
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DR EMBL; X54915; CA438687.1; -.
DR PIR; S14275; S14275.
DR HSSP; P14779; IJPE2.
DR GO; GO:0005624; C:membrane fraction; ISS.
DR GO; GO:0004497; P:monooxygenase activity; ISS.
DR GO; GO:0006805; P:xenobiotic metabolism; ISS.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR008072; EP450_CYP3A.
DR InterPro; IPR002401; EP450I.
DR Pfam; PF00067; P450_1.
DR PRINTS; PR00463; EP450I.
DR PRINTS; PR01689; EP450IICYP3A.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Electron transport; Endoplasmic reticulum; Heme; Membrane; Microsome;
KW Monooxygenase; Oxidoreductase.
FT METAL 442 442 Iron (heme axial ligand) (By similarity).
SQ SEQUENCE 503 AA; 57721 MW; 52171D03F9BDS87 CRC64;

Query Match 81.7%; Score 2077; DB 1; Length 503;
Best Local Similarity 79.7%; Pred. No. 3.5e-143;
Matches 382; Conservative 55; Mismatches 42; Indels 0; Gaps 0;

QY 3 YGTHSHGLFKKLGIPGPTLPFLGNILSYHKFCMFDMCHKYKGVNGFYDGOQPVLA1 62
DB 25 YGTHSHGLFKKLGIPGPTLPFLGNILSYRQGLMKFPDTECYKKGKMMRTQDQLPVLRT 84
QY 63 TDDDMIKTVLVKCYSVFTNRRPFGVGFMSKSAISIAEDDEMRKLSLSPTTSGLKE 122
DB 85 TDDDMIKTVLVKCYSVFTNRRPFGVGFMSKSAISIAEDDEMRKLSLSPTTSGLKE 144
QY 123 MVEPIIAQYGDVAVRNLRAREATGKPVTLKDVFGAYSMDVITTSFGVNIIDSLNPPDPPV 182
DB 145 MPEPIIAQYGDVAVRNLRAREATGKPVTLKDVFGAYSMDVITTSFGVNIIDSLNPPDPPV 204
QY 183 ENTCKLRFDPDLPFLSTIVFPFLIPLEVLNIVCPREAVTNPLKSKYRMKESRLDET 242
DB 205 ENTCKLRFDPDLPFLSTIVFPFLIPLEVLNIVCPREAVTNPLKSKYRMKESRLDET 264
QY 243 QKRHVDFLOQIMDSQNSKETESHKALSDLELVAOSIIFIPAGYETTSVLSFIYBLATH 302

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Db 265 QKRVDFLOLMINSQSKENDTHKALSDLELVAOSIIFAGYETTSTSLFMYELATH 324
QY 303 PDVOQKLOEIEDALFPAKAPPTVTVLQMEYLDVNVNETLRLEPIAMLERVCKVDYIN 362
Db 325 PDVOQKLOEIEDALFPAKAPPTVTVLQMEYLDVNVNETLRLEPIAMLERVCKVDYIN 384
QY 363 GMFIPKGVVVMIPSYALHBPCKWTBEPKFLPERFSKKNKNDIDPYLYTPFGSPRNCIG 422
Db 385 GVFIPIKGTVMVVFPIHROSLMPBEBEPERFSKKNKNDIDPYLYTPFGSPRNCIG 444
QY 423 MRPALNMKALIRVLQNFSPKCKEQTQIPKLSLGLLOPEKPVVLKVESRDGTSGA 481
Db 445 MRPALNMKALIRVLQNFSPKCKEQTQIPKLSLGLLOPEKPVVLKVESRDGTSGA 503
RESULT 14
ID Q8HZK1 PRELIMINARY; PRT; 503 AA.
AC Q8HZK1;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Cytochrome P450 3A26.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Plissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98064129; PubMed=9400018;
RA Fraser D.J., Feyereisen R., Harlow G.R., Halpert J.R.;
RT "Isolation, heterologous expression and functional characterization of
a novel cytochrome P450 3A enzyme from a canine liver cDNA library."
RT J. Pharmacol. Exp. Ther. 283:1425-1432(1997).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Fraser D.J., Feyereisen R., Harlow G.R., Halpert J.R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AF547269; AA047145.1; -.
DR HSSP; P14779; IUPZ.
DR GO; GO:0005624; C:membrane fraction; ISS.
DR GO; GO:0004497; F:monooxygenase activity; ISS.
DR GO; GO:0006805; P:xenobiotic metabolism; ISS.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002407; EP4501.
DR InterPro; IPR008072; EP450_CYP3A.
DR Pfam; PF00067; P450_1.
DR PRINTS; PR00463; EP4501.
DR PRINTS; PR01689; EP4501CYP3A.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KM Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 503 AA; 57726 MW; AFBG6002CCTCA67 CRC64;

Query Match 79.7%; Score 2025; DB 2; Length 503;
Best Local Similarity 77.9%; Pred. No. 2.2e-139;
Matches 373; Conservative 57; Mismatches 49; Indels 0; Gaps 0;

QY 3 YGTHSHGLFKKGLIPGTPPLPGNLISYHKGFMFMMECHKYKQKMGYDGOQPLAT 62
Db 25 YGTYTHGIFRKLGIPTPLPFGVTAAGYNGFVPMKCFKXGRMGFYDGRQPLAT 84
QY 63 TDDMDIKTVLVKSCYSFTNRPRPGVGFPMKSAISIDEDEWKRRLSLPTFTSGDLKE 122
Db 85 TDDMDIKTVLVKSCYSFTNRPRPGVGFPMKSAISIDEDEWKRRLSLPTFTSGDLKE 144
QY 123 MVDPIAQGVDLVNRIRREAEKSPVTLKQVFGAYSMDVITSTFGVNIDSLNPPDPFV 182
Db 145 MPPIIGYGVDLVNRIRREAEKSPVTLKQVFGAYSMDVITSTFGVNIDSLNPPDPFV 204

QY 183 ENTKKLRFDFLPFPLSITVPPFLPILEVLNICEPREVTNFKSVKMKSRLEDT 242
Db 205 ENTKKLRFDFLPFPLSITVPPFLPILEVLNICEPREVTNFKSVKMKSRLEDT 264
QY 243 QKRVDFLOLMINSQSKENDTHKALSDLELVAOSIIFAGYETTSTSLFMYELATH 302
Db 265 QKRVDFLOLMINSQSKENDTHKALSDLELVAOSIIFAGYETTSTSLFMYELATH 324
QY 303 PDVOQKLOEIEDALFPAKAPPTVTVLQMEYLDVNVNETLRLEPIAMLERVCKVDYIN 362
Db 325 PDVOQKLOEIEDALFPAKAPPTVTVLQMEYLDVNVNETLRLEPIAMLERVCKVDYIN 384
QY 363 GMFIPKGVVVMIPSYALHBPCKWTBEPKFLPERFSKKNKNDIDPYLYTPFGSPRNCIG 422
Db 385 GVFIPIKGTVMVVFPIHROSLMPBEBEPERFSKKNKNDIDPYLYTPFGSPRNCIG 444
QY 423 MRPALNMKALIRVLQNFSPKCKEQTQIPKLSLGLLOPEKPVVLKVESRDGTSGA 481
Db 445 MRPALNMKALIRVLQNFSPKCKEQTQIPKLSLGLLOPEKPVVLKVESRDGTSGA 503
RESULT 15
ID CP39 RAT STANDARD; PRT; 503 AA.
AC P51538; 064557; 064631;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cytochrome P450 3A9 (EC 1.14.14.1) (CYP3A9) (P450-OLFA) (Olfactive)
DE (3AH15).
GN Name=Cyp3a9;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Braque-Dawley;
RX MEDLINE=9714501; PubMed=8990268; DOI=10.1006/abbi.1996.9752;
RA Mahne A., Strotkamp D., Roos P.H., Hanstein W.G., Chabot G.G.,
RA Neff P.;
RT "Expression and inducibility of cytochrome P450 3A9 (CYP3A9) and other
members of the CYP3A subfamily in rat liver."
RT Arch. Biochem. Biophys. 337:62-68(1997).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96220175; PubMed=8660328; DOI=10.1006/bbrc.1996.0562;
RA Wang H., Kawashima H., Strobel H.W., rat brain."
RL Biochem. Biophys. Res. Commun. 221:157-162(1996).
CC -1- FUNCTION: This isozyme seems to be implicated in olfaction. Active
in the demethylation of erythromycin as well as benzphetamine.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- TISSUE SPECIFICITY: Mainly expressed in olfactory epithelium.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
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or send an email to license@isb-sib.ch).
CC EMBL; U60085; AAB03662.1; -.
DR EMBL; U60085; AAB03662.1; -.
DR PIR; JC4702; JC4702.
DR HSSP; P14779; IUPZ.
DR GO; GO:0005624; C:membrane fraction; ISS.
DR GO; GO:0004497; F:monooxygenase activity; ISS.

CC to generate an electron density map of 3A4 crystal structures as given in
CC specification and constructing an electron density map of the structural
CC factors and phases. The method of the invention has cytochrome
CC applications and may be useful for obtaining a representation of the 3-
CC dimensional structure of a crystal of CYP3A4, where the crystal structure
CC is useful in modelling the interaction of a compound with the protein and
CC in drug design. Such information may be utilised on order to generate a
CC composition to treat cancer. The current sequence is that of the human
CC CYP3A4 N-terminal truncated protein of the invention which has a
CC synthetic N-terminal region in place of the hydrophobic transmembrane
CC domain in order to aid Escherichia coli expression and solubility, in
CC addition to a C-terminal His tag which facilitates purification.

XX
XX
SQ Sequence 485 AA;

Query Match 100.0%; Score 2542; DB 8; Length 485;
Best Local Similarity 100.0%; Pred. No. 7.2e-230;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFQCMFMECHKKYGKVGWGYDGOQPVYL 60
DB 1 MAYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFQCMFMECHKKYGKVGWGYDGOQPVYL 60
QY 61 AITDPMIKTVLVKECYSVFTNRRPGVGFPMKSAISIADEBWKRLSLSPFTSGKL 120
DB 61 AITDPMIKTVLVKECYSVFTNRRPGVGFPMKSAISIADEBWKRLSLSPFTSGKL 120
QY 121 KEMVPIIAQYGDVLVRLNLRREAEKGKVTLKDVFGAYSMDVITSTSGVNIIDSLNPNOP 180
DB 121 KEMVPIIAQYGDVLVRLNLRREAEKGKVTLKDVFGAYSMDVITSTSGVNIIDSLNPNOP 180
QY 181 FVENTKKLRFDFLDPFLSTIVFPFLPILEVLNLCVPREVTNFRKSVKMKESRL 240
DB 181 FVENTKKLRFDFLDPFLSTIVFPFLPILEVLNLCVPREVTNFRKSVKMKESRL 240
QY 241 DTQKRVDFLOLMIDSONSKETESHKALSDLELVAOSIIFIFAGYETTSSVLSFIWYELA 300
DB 241 DTQKRVDFLOLMIDSONSKETESHKALSDLELVAOSIIFIFAGYETTSSVLSFIWYELA 300
QY 301 THPDVQOKLOEIEIDAVLPNKAPPTVDVLOMEYLDWVNVETLRLPIAMRLERVCKDVE 360
DB 301 THPDVQOKLOEIEIDAVLPNKAPPTVDVLOMEYLDWVNVETLRLPIAMRLERVCKDVE 360
QY 361 INGMFIPKGVVVMIPSYALHRDPKYTEPEKFLPERFSKKNKONIDPIYITPFGSGPRNC 420
DB 361 INGMFIPKGVVVMIPSYALHRDPKYTEPEKFLPERFSKKNKONIDPIYITPFGSGPRNC 420
QY 421 IGMRFALMMKALALIRVLQNFSPKCKETOIPLKLSLGLLOPEKPVVLKVESRDGTVSG 480
DB 421 IGMRFALMMKALALIRVLQNFSPKCKETOIPLKLSLGLLOPEKPVVLKVESRDGTVSG 480

QY 481 AHHHH 485
DB 481 AHHHH 485

RESULT 2

ADJ87521 standard; protein; 485 AA.

ID ADJ87521
AC ADJ87521;
DT 06-MAY-2004 (first entry)
XX Human cytochrome P450 3A4 protein.
XX Human cytochrome P450 3A4 protein.
XX cytochrome P450; crystallography.
XX Homo sapiens.
OS Unidentified.
XX
XX MO2003102192-A1.
XX

PD 11-DEC-2003.
XX
PF 30-MAY-2002; 2002MO-GB002668.
XX
PR 30-MAY-2002; 2002MO-GB002668.
XX
PA (ASTE-) ASTEX TECHNOLOGY LTD.
XX
PI Cosme J, Ward A, Villard L, Williams P, Hamilton B;
XX
DR WPI; 2004-04319/04.
DR N-PSDB; ADJ87520.
XX
PT Purifying a cytochrome P450, for NMR studies and high-throughput
PT screening methods to discover drugs, comprises suspending cells
PT expressing P450 molecule in a salt buffer, lysing the cells and providing
PT a high-salt-detergent lysate.
XX
PS Claim 12; SEQ ID NO 8; 77pp; English.

CC The invention relates to a method of purifying a cytochrome P450 by
CC expressing in a host cell culture a cytochrome P450 molecule, recovering
CC the cells from the culture and suspending the cells in a salt buffer
CC having a conductivity of 12-110 mS/cm, lysing the cells and removing cell
CC debris to provide a high-salt lysate, adding to the lysate a detergent to
CC provide a high-salt-detergent lysate, and recovering the P450 from the
CC lysate. Methods of preparing and purifying cytochrome P450 proteins are
CC useful for X-ray crystallographic studies and crystallographic screening
CC of small molecules bound to P450, or for NMR studies and high-throughput
CC screening methods to discover drugs or analyze the interaction of drugs
CC with P450 molecules. This sequence corresponds to the human cytochrome
CC P450 3A4.
XX
XX

SQ Sequence 485 AA;

Query Match 99.6%; Score 2533; DB 8; Length 485;
Best Local Similarity 99.8%; Pred. No. 5e-229;
Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFQCMFMECHKKYGKVGWGYDGOQPVYL 60
DB 1 MAYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFQCMFMECHKKYGKVGWGYDGOQPVYL 60
QY 61 AITDPMIKTVLVKECYSVFTNRRPGVGFPMKSAISIADEBWKRLSLSPFTSGKL 120
DB 61 AITDPMIKTVLVKECYSVFTNRRPGVGFPMKSAISIADEBWKRLSLSPFTSGKL 120
QY 121 KEMVPIIAQYGDVLVRLNLRREAEKGKVTLKDVFGAYSMDVITSTSGVNIIDSLNPNOP 180
DB 121 KEMVPIIAQYGDVLVRLNLRREAEKGKVTLKDVFGAYSMDVITSTSGVNIIDSLNPNOP 180
QY 181 FVENTKKLRFDFLDPFLSTIVFPFLPILEVLNLCVPREVTNFRKSVKMKESRL 240
DB 181 FVENTKKLRFDFLDPFLSTIVFPFLPILEVLNLCVPREVTNFRKSVKMKESRL 240
QY 241 DTQKRVDFLOLMIDSONSKETESHKALSDLELVAOSIIFIFAGYETTSSVLSFIWYELA 300
DB 241 DTQKRVDFLOLMIDSONSKETESHKALSDLELVAOSIIFIFAGYETTSSVLSFIWYELA 300
QY 301 THPDVQOKLOEIEIDAVLPNKAPPTVDVLOMEYLDWVNVETLRLPIAMRLERVCKDVE 360
DB 301 THPDVQOKLOEIEIDAVLPNKAPPTVDVLOMEYLDWVNVETLRLPIAMRLERVCKDVE 360
QY 361 INGMFIPKGVVVMIPSYALHRDPKYTEPEKFLPERFSKKNKONIDPIYITPFGSGPRNC 420
DB 361 INGMFIPKGVVVMIPSYALHRDPKYTEPEKFLPERFSKKNKONIDPIYITPFGSGPRNC 420
QY 421 IGMRFALMMKALALIRVLQNFSPKCKETOIPLKLSLGLLOPEKPVVLKVESRDGTVSG 480
DB 421 IGMRFALMMKALALIRVLQNFSPKCKETOIPLKLSLGLLOPEKPVVLKVESRDGTVSG 480
QY 481 AHHHH 485
DB 481 AHHHH 485

Db 481 AHFH 485

RESULT 3
ABG68753
ID ABG68753 standard; protein; 503 AA.

XX
AC ABG68753;
XX
DT 07-OCT-2002 (first entry)

XX
DE Cytochrome P450 CYP3A43 exon 1-CYP3A4 exon 2-13.

XX
KM Cytochrome P450; CYP3A41; CYP3A42; CYP3A43; CYP3A4; CYP3A5; CYP3A7;
KW drug metabolism; drug design; drug screening.

XX
OS Homo sapiens.

XX
PN WO200244213-A1.

XX
PD 06-JUN-2002.

XX
PF 28-NOV-2001; 2001WO-SE002631.

XX
PR 28-NOV-2000; 2000SE-00004366.

XX
PR 11-JUN-2001; 2001SE-00002061.

XX
PA (ZAPR/) ZAPHIROPOULOS P G.
XX (FINT/) FINTA C.

XX
PI Zaphiropoulos PG, Finta C;
XX
DR WPI; 2002-557532/59.
DR N-PSDB; ABK97692.

XX
PT Novel cytochrome P450 protein in which CYP3A43 exon 1 is joined to sets
PT of CYP3A4 or CYP3A5 exons, useful as medicament, and in evaluating drug
PT metabolism, in drug design and drug screening.

XX
PS Claim 2, Fig 11, 131pp; English.

XX
CC The invention describes a cytochrome P450 protein (I) in which CYP3A43
CC exon 1 is joined to sets of CYP3A4 or CYP3A5 exons, as well as sub
CC fragments, variants and multiples of (I) having essentially the same
CC characteristics. (I) is useful as a medicament, and for evaluating drug
CC metabolism, in drug design, and drug screening, and in tests for
CC adjusting the dose of drugs. This is the amino acid sequence of a novel
CC cytochrome P450 protein

XX
SQ Sequence 503 AA;

Query Match 98.4%; Score 2501; DB 5; Length 503;
Best Local Similarity 100.0%; Pred. No. 5,4e-226;
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YGTHSHLFFKRLGIPGPTPLPFLGNITISYHKGFCMFMECHKKKYKXWGPIDGQOPLAI 62
DB 25 YGTHSHLFFKRLGIPGPTPLPFLGNITISYHKGFCMFMECHKKKYKXWGPIDGQOPLAI 84

QY 63 TDDPMIKTVLVEKCYVFTNRPRPGVGFPMKSAISIADEBEKRLRSLSTPTPSGLAKE 122
DB 85 TDDPMIKTVLVEKCYVFTNRPRPGVGFPMKSAISIADEBEKRLRSLSTPTPSGLAKE 144

QY 123 MVLPIAGYGVLVNLRREAEATGKPVTLKOVFGAYSMDVITSTSGVNIIDSLNPPDPFV 182
DB 145 MVLPIAGYGVLVNLRREAEATGKPVTLKOVFGAYSMDVITSTSGVNIIDSLNPPDPFV 204

QY 183 ENTKKLIRPFLDPFISTVFPPLIPILVLANICVPRRYTNLAKSVKMKESRLDET 242
DB 205 ENTKKLIRPFLDPFISTVFPPLIPILVLANICVPRRYTNLAKSVKMKESRLDET 264

QY 243 QKRVDFLQIMIDSONSKETESHKALSDLELVAGSIIFIFAGYETTSVLSFIYELATH 302

Db 265 QKRVDFLQIMIDSONSKETESHKALSDLELVAGSIIFIFAGYETTSVLSFIYELATH 324

QY 303 PDVQOKLQSEIDAVLPKAPPTDTVLQMEYLDVNVNLTALPFIANLEBCKKDVAIN 362
DB 325 PDVQOKLQSEIDAVLPKAPPTDTVLQMEYLDVNVNLTALPFIANLEBCKKDVAIN 384

QY 363 GMPIPKGVVMMIPSYALHRDPKWTPEBEKLPFRFSKKNNDIDPYLYTPGSGPRNCIG 422
DB 385 GMPIPKGVVMMIPSYALHRDPKWTPEBEKLPFRFSKKNNDIDPYLYTPGSGPRNCIG 444

QY 423 MRFALMMKALIRVLQNFSPCKETQIPKLSIGLQPEKPVVLKVESRDGTSGA 481
DB 445 MRFALMMKALIRVLQNFSPCKETQIPKLSIGLQPEKPVVLKVESRDGTSGA 503

RESULT 4
ABUS7260
ID ABUS7260 standard; protein; 503 AA.

XX
AC ABUS7260;
XX
DT 25-APR-2003 (first entry)

XX
DE Human chytochrome P450 CYP3A4 protein.

XX
KM Human; enzyme; transgenic; drug metabolism; behaviour; mouse;
KW pharmacokinetic assay; pharmacodynamic assay; toxicology; serum albumin;
KW alpha-acidic glycoprotein; CYP; multidrug resistance protein; MRP;
KW uridine diphosphoglucuronosyl transferase; UGT; cytochrome P450.

XX
OS Homo sapiens.

XX
PN WO200283897-A1.

XX
PD 24-OCT-2002.

XX
PF 18-APR-2002; 2002WO-AU000485.

XX
PR 18-APR-2001; 2001AU-00004467.

XX
PA (GENE-) GENE STREAM PTY LTD.

XX
PI Daly JM;
XX
DR WPI; 2003-093021/08.
DR N-PSDB; ABX77172.

XX
PT New transgenic non-human animal expressing a foreign polypeptide
PT associated with drug behavior and/or metabolism, useful for studying the
PT behavior and/or metabolism of a drug in other animals.

XX
PS Disclosure; Page 299-301; 408pp; English.

XX
CC This invention relates to a transgenic non-human animal which may be used
CC for assessing the behaviour and/or metabolism of a drug in another animal
CC and which expresses a foreign polypeptide associated with drug behaviour
CC and/or metabolism. The invention also comprises a nucleic acid construct
CC for use in producing the above transgenic non-human animal and a method
CC of assessing the metabolism and/or behavior of a drug in an animal of
CC interest, comprising administering a test agent to the transgenic animal
CC and conducting analytical tests to determine drug metabolism and/or
CC behaviour. The transgenic animal is useful in studying drug metabolism
CC in producing the above transgenic animal and the methods are used for
CC (e.g. pharmacokinetic or pharmacodynamic assays) and/or toxicological
CC studies. Nucleic acid sequences used within the invention are serum
CC albumin; alpha-acidic glycoprotein; cytochrome P450 (CYP); uridine
CC diphosphoglucuronosyl transferase (UGT); multidrug resistance proteins
CC and (MRP's). The present sequence represents a protein sequence used to
CC create a transgenic animal within the scope of the invention

XX
SQ Sequence 503 AA;

Query Match 98.4%; Score 2501; DB 6; Length 503;
Best Local Similarity 100.0%; Pred. No. 5.4e-226;
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YGTHSHGLPKKGIIGPTPLPFLGNILSYHKGFCMFDECHCKYKGVWGFGYDQGPVLAI 62
DB 25 YGTHSHGLPKKGIIGPTPLPFLGNILSYHKGFCMFDECHCKYKGVWGFGYDQGPVLAI 84
QY 63 TDPDMIKTVLVKECYVFTNRRPFGVGFMSKAIISIAEDBEKRLRLSLPTFTSGKLKE 122
DB 85 TDPDMIKTVLVKECYVFTNRRPFGVGFMSKAIISIAEDBEKRLRLSLPTFTSGKLKE 144
QY 123 MWPILIAQYGDVLRNLRREAETGKPYTLKDVFGASMDVITSTSGVNIIDSLNPDPPV 182
DB 145 MWPILIAQYGDVLRNLRREAETGKPYTLKDVFGASMDVITSTSGVNIIDSLNPDPPV 204
QY 183 ENTKKLIRPDLDPFLSLITVPFPLIPILEVNIICVFPREVTFNRKSVKMKESRLBDT 242
DB 205 ENTKKLIRPDLDPFLSLITVPFPLIPILEVNIICVFPREVTFNRKSVKMKESRLBDT 264
QY 243 QKRVDFLOLMIDSONSKETESHKALSDLEVAQSIIFIFAGYETTSVLSTIMELATH 302
DB 265 QKRVDFLOLMIDSONSKETESHKALSDLEVAQSIIFIFAGYETTSVLSTIMELATH 324
QY 303 PDVQOKLQGEIDAVLPNKAPPTYDTVLQMEYLDVMVNETLRLEPIAMRLERYCKDVEIN 362
DB 325 PDVQOKLQGEIDAVLPNKAPPTYDTVLQMEYLDVMVNETLRLEPIAMRLERYCKDVEIN 384
QY 363 GMFIPKGVVMMIPSYALHRDPKYWTEPEKFLPERFSKKNKNDIDPIYITPFGSGPRNCIG 422
DB 385 GMFIPKGVVMMIPSYALHRDPKYWTEPEKFLPERFSKKNKNDIDPIYITPFGSGPRNCIG 444
QY 423 MRFALNMKALIRVLQNFSPFKCKETOIPLKLSIGLLQPEKPVVLKVESRDGTVSGA 481
DB 445 MRFALNMKALIRVLQNFSPFKCKETOIPLKLSIGLLQPEKPVVLKVESRDGTVSGA 503

RESULT 5
ABR82024
ID ABR82024 standard; protein; 503 AA.
XX
AC ABR82024;
XX
DT 22-SEP-2003 (first entry)
XX
DE Human cytochrome P450 3A4 amino acid sequence.
XX
KW Human; protein array; protein moiety; phenotype; drug discovery;
KW naturally occurring variant; pharmacogenomic; diagnostic;
KW parallel analysis; tumour suppressor; p53; cytochrome P450.
XX
OS Homo sapiens.
XX
PN WO2003048768-A2.
XX
PD 12-JUN-2003.
XX
PF 05-DEC-2002; 2002WO-GB005499.
XX
PR 05-DEC-2001; 2001US-0335806P.
XX
PR 16-SEP-2002; 2002US-0410815P.
XX
PA (SENS-) SENSE PROTEOMIC LTD.
XX
PI Bouteil JM, Godber BLJ, Hart DJ, Blackburn JD;
XX
XX WPI; 2003-569063/53.
XX
XX DR N-PSDB; ACP06054.
XX
XX PT New protein array, useful for determining the phenotype of a naturally
XX occurring variant of a DNA sequence of interest, comprises a surface upon
XX PT which at least two protein moieties are deposited.

XX
PS Example 5; Fig 11B; 84pp; English.
XX
CC The present invention describes a protein array comprising a surface upon
CC which at least two protein moieties are deposited at spatially defined
CC locations, where the protein moieties are naturally occurring variants of
CC a DNA sequence of interest. Also described: (1) making a protein array;
CC (2) screening a set of protein moieties for molecules that interact with
CC one or more proteins; and (3) simultaneously determining the relative
CC properties of members of a set of protein moieties. The protein array can
CC be used for determining the phenotype of a naturally occurring variant of
CC a DNA sequence of interest. The protein array is useful for drug
CC discovery, pharmacogenomics and diagnostics. The protein array allows the
CC parallel analysis of closely related proteins with a sensitivity that is
CC at least comparable to existing methods, if not better, with small
CC volumes of potentially expensive ligands, and in a quantitative,
CC comparative functional analysis manner not previously possible. ACP06000
CC to ACP06056 and ABR81975 to ABR82026 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 503 AA;
Query Match 98.4%; Score 2501; DB 6; Length 503;
Best Local Similarity 100.0%; Pred. No. 5.4e-226;
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YGTHSHGLPKKGIIGPTPLPFLGNILSYHKGFCMFDECHCKYKGVWGFGYDQGPVLAI 62
DB 25 YGTHSHGLPKKGIIGPTPLPFLGNILSYHKGFCMFDECHCKYKGVWGFGYDQGPVLAI 84
QY 63 TDPDMIKTVLVKECYVFTNRRPFGVGFMSKAIISIAEDBEKRLRLSLPTFTSGKLKE 122
DB 85 TDPDMIKTVLVKECYVFTNRRPFGVGFMSKAIISIAEDBEKRLRLSLPTFTSGKLKE 144
QY 123 MWPILIAQYGDVLRNLRREAETGKPYTLKDVFGASMDVITSTSGVNIIDSLNPDPPV 182
DB 145 MWPILIAQYGDVLRNLRREAETGKPYTLKDVFGASMDVITSTSGVNIIDSLNPDPPV 204
QY 183 ENTKKLIRPDLDPFLSLITVPFPLIPILEVNIICVFPREVTFNRKSVKMKESRLBDT 242
DB 205 ENTKKLIRPDLDPFLSLITVPFPLIPILEVNIICVFPREVTFNRKSVKMKESRLBDT 264
QY 243 QKRVDFLOLMIDSONSKETESHKALSDLEVAQSIIFIFAGYETTSVLSTIMELATH 302
DB 265 QKRVDFLOLMIDSONSKETESHKALSDLEVAQSIIFIFAGYETTSVLSTIMELATH 324
QY 303 PDVQOKLQGEIDAVLPNKAPPTYDTVLQMEYLDVMVNETLRLEPIAMRLERYCKDVEIN 362
DB 325 PDVQOKLQGEIDAVLPNKAPPTYDTVLQMEYLDVMVNETLRLEPIAMRLERYCKDVEIN 384
QY 363 GMFIPKGVVMMIPSYALHRDPKYWTEPEKFLPERFSKKNKNDIDPIYITPFGSGPRNCIG 422
DB 385 GMFIPKGVVMMIPSYALHRDPKYWTEPEKFLPERFSKKNKNDIDPIYITPFGSGPRNCIG 444
QY 423 MRFALNMKALIRVLQNFSPFKCKETOIPLKLSIGLLQPEKPVVLKVESRDGTVSGA 481
DB 445 MRFALNMKALIRVLQNFSPFKCKETOIPLKLSIGLLQPEKPVVLKVESRDGTVSGA 503

RESULT 6
ADL18578
ID ADL18578 standard; protein; 503 AA.
XX
AC ADL18578;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human wild-type cytochrome P450 CYP3A4 protein.
XX
XX KW drug metabolic activity; CYP3A4; human; wild-type; cytochrome P450; SNP;
XX KW single nucleotide polymorphism.
XX
XX OS Homo sapiens.

XX Key Location/Qualifiers
 FH Misc-difference 185 /note= "Thr may be substituted for Ser due to single
 FT nucleotide polymorphism (SNP) in coding DNA"
 FT Misc-difference 293 /note= "Leu may be substituted for Pro due to single
 FT nucleotide polymorphism (SNP) in coding DNA"
 FT Misc-difference 363 /note= "Thr may be substituted for Met due to single
 FT nucleotide polymorphism (SNP) in coding DNA"
 XX JP2004000004-A.
 XX PD 08-JAN-2004.
 XX PE 23-APR-2002; 2002JP-00120246.
 XX PR 23-APR-2002; 2002JP-00120246.
 XX (HOKU-) KOKURITSU IYAKUJIN SHOKUJIN EISEI KENKUU.
 XX (IYAK-) IYAKUJIN FUKUSAYO HIGAI KYUSAI KENKUU SH.
 XX WPI; 2004-085203/09.
 XX DR N-PSDB; ADL18577.
 XX PT Testing the drug metabolic activity of CYP3A4 such as testosterone
 PT hydroxylase activity by detecting the CYP3A4 gene polymorphisms in which
 PT the drug metabolic activity of CYP3A4 is reduced.
 XX PS Disclosure; SEQ ID NO 2; 48bp; Japanese.
 CC The invention relates to a novel method for testing the drug metabolic
 CC activity of CYP3A4 by detecting the CYP3A4 gene polymorphisms in which
 CC the drug metabolic activity of CYP3A4 is reduced. The method of the
 CC invention may be useful for testing the possibility of a side effect
 CC resulting from a drug metabolised by CYP3A4 in a subject. The current
 CC sequence is that of the human wild-type cytochrome P450 CYP3A4 protein of
 CC the invention.
 XX SQ Sequence 503 AA;
 Query Match 98.4%; Score 2501; DB 8; Length 503;
 Best Local Similarity 100.0%; Pred. No. 5.4e-226;
 Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMPDMECHKYKVGWGFYDGGQPVLA1 62
 DB 25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMPDMECHKYKVGWGFYDGGQPVLA1 84
 QY 63 TDDPMITVLYKCYVFTNRRPPGVGFMKSAISIADEBEWKLRSLSPFTSGKLKE 122
 DB 85 TDDPMITVLYKCYVFTNRRPPGVGFMKSAISIADEBEWKLRSLSPFTSGKLKE 144
 QY 123 MNPVIAQGVLYNLRBAETGKPYLKVDFGYSMDVITSTSGNINISINNPDPFV 182
 DB 145 MNPVIAQGVLYNLRBAETGKPYLKVDFGYSMDVITSTSGNINISINNPDPFV 204
 QY 183 ENTKKLARFDFLPFLSTIVFPFLIPILEVLANICVPPREVTNLRKSVKMKESRLDET 242
 DB 205 ENTKKLARFDFLPFLSTIVFPFLIPILEVLANICVPPREVTNLRKSVKMKESRLDET 264
 QY 243 QKRRVDFLOMIDSONSKETESHKALSDLEIVAOSIIFRAGYETTSVLSFIWYELATH 302
 DB 265 QKRRVDFLOMIDSONSKETESHKALSDLEIVAOSIIFRAGYETTSVLSFIWYELATH 324
 QY 303 PDVQOKLOEERIDAVLPKAPETVDTVLOMEYLDVNVNMTLRPPIARLERVCKQDVEN 362
 DB 325 PDVQOKLOEERIDAVLPKAPETVDTVLOMEYLDVNVNMTLRPPIARLERVCKQDVEN 384
 QY 363 GMFIPKGVVMMISYALHRDPKWTBEPKFLPERFSKKNNDIDPIYTFPGSGPRNCIG 422
 DB 385 GMFIPKGVVMMISYALHRDPKWTBEPKFLPERFSKKNNDIDPIYTFPGSGPRNCIG 444

QY 423 MRPALMMKALIRVLONFSPKPKCKEIOIPKLISGLGLDPEKPVNLKVESROCTVSGA 481
 DB 445 MRPALMMKALIRVLONFSPKPKCKEIOIPKLISGLGLDPEKPVNLKVESROCTVSGA 503
 RESULT 7
 ADL18672
 ID ADL18672 standard; protein; 503 AA.
 AC ADL18672;
 DT 17-JUN-2004 (first entry)
 DE Human cytochrome P450 enzyme 3A4 protein.
 KW protein array; protein moiety; drug metabolising enzyme; DME;
 KW drug metabolism; drug toxicity; cytotoxicity; drug metabolite;
 KW metabolic pathway; human; cytochrome; enzyme; P450.
 OS Homo sapiens.
 XX WO2004025244-A2.
 XX PD 25-MAR-2004.
 XX PE 16-SEP-2003; 2003WO-IB005258.
 XX PR 16-SEP-2002; 2002US-0410815P.
 XX PR 05-DEC-2002; 2002US-00313963.
 XX PR 05-DEC-2002; 2002WO-GB005499.
 XX (SENS-) SENSE PROTEOMIC LTD.
 XX PI Boutell JM, Godber BLJ, Hart DJ, Bockett NA, Kozlowski R;
 XX WPI; 2004-270121/25.
 XX DR N-PSDB; ADL18671.
 DR New protein array comprising a surface having spatially defined locations
 PT containing drug metabolizing enzymes, examining gender and ethnicity-
 PT related differences in drug metabolism or cytotoxicity of drug
 PT metabolites.
 XX PS Example 3; Fig 3B; 72pp; English.
 CC The present invention describes a protein array comprising a surface
 CC having spatially defined locations where at each location there are
 CC deposited at least two protein moieties capable of forming a complex,
 CC where the complex is transiently formed and where the protein moieties
 CC act sequentially on a substrate of interest and are derived from one or
 CC more drug metabolising enzymes (DMEs). Also described: (1) a method of
 CC making a protein array; (2) an array made by the method of (1); (3) a
 CC method of screening a set of protein moieties for molecules which
 CC interact with one or more proteins; (4) a method of simultaneously
 CC determining the relative properties of members of a set of protein
 CC moieties; and (5) a method of expressing and purifying a DME. The protein
 CC array is useful in examining gender differences in drug metabolism,
 CC ethnicity-related differences in drug metabolism and toxicity between two
 CC or more mammalian species, e.g. human and rat and cytotoxicity of drug
 CC metabolites, in defining and quantifying metabolic pathways for small
 CC molecules, in screening of compounds that binds and inhibits individual
 CC DMEs and in analysing induction of P450 expression by one or more
 CC compounds of interest and the effects of mutation on the activity of a
 CC DME of interest. The present sequence represents human cytochrome P450
 CC enzyme 3A4, which is used in the exemplification of the present
 CC invention.
 XX SQ Sequence 503 AA;
 Query Match 98.4%; Score 2501; DB 8; Length 503;
 Best Local Similarity 100.0%; Pred. No. 5.4e-226;
 Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 3 YGTHSHGLFKKLGIGPPTPLPFLGNILSYHKGFCEMDECHKKYGVWGFYDGOQPVLA1 62
DB 25 YGTHSHGLFKKLGIGPPTPLPFLGNILSYHKGFCEMDECHKKYGVWGFYDGOQPVLA1 84
QY 63 TDPDMIKTVLVKCYSVFTNRRPFGVGFEMKSAISIAEDEMKRLRSLSPFTSGKLKE 122
DB 85 TDPDMIKTVLVKCYSVFTNRRPFGVGFEMKSAISIAEDEMKRLRSLSPFTSGKLKE 144
QY 123 MVEPIAQYGDVAVRNLRREAETGKPYTLKDVFGAYSMDVITSTSPGVNIDSLNPPDPV 182
DB 145 MVEPIAQYGDVAVRNLRREAETGKPYTLKDVFGAYSMDVITSTSPGVNIDSLNPPDPV 204
QY 183 ENTKKLRRPFLDPFLSTVFPFLPILEVANI CVPREVTNFKRSYKRMKESRLDET 242
DB 205 ENTKKLRRPFLDPFLSTVFPFLPILEVANI CVPREVTNFKRSYKRMKESRLDET 264
QY 243 OKHRVDFLOLMDSONSKETESHKALSDLELVAQSIIFIPAGYETTSVLSFIMYELATH 302
DB 265 OKHRVDFLOLMDSONSKETESHKALSDLELVAQSIIFIPAGYETTSVLSFIMYELATH 324
QY 303 PDVQOQLQOEIDAVLPNKAPPTVDVLOMEYLDVMVNETLRFPAMRLERCKKQVEIN 362
DB 325 PDVQOQLQOEIDAVLPNKAPPTVDVLOMEYLDVMVNETLRFPAMRLERCKKQVEIN 384
QY 363 GMFIPKGVVMMIPSYALHDPKWTBPEKFLPERFSKKNDIDPIYITPFGSGPRNCIG 422
DB 385 GMFIPKGVVMMIPSYALHDPKWTBPEKFLPERFSKKNDIDPIYITPFGSGPRNCIG 444
QY 423 MRFALNMKTLALIRVLQNSFPKCKETQIPLKLSLGILLQPEKPVVLKYESRDGTVSGA 481
DB 445 MRFALNMKTLALIRVLQNSFPKCKETQIPLKLSLGILLQPEKPVVLKYESRDGTVSGA 503

RESULT 8
ADD48378
ID ADD48378 standard; protein; 502 AA.
XX
AC ADD48378;
XX
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Human Protein A29815, SEQ ID NO 14079.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
OS unidentified.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002MO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333477P.
XX
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
PI Woolf C, D'urso D, Befort K, Costigan M,
XX
XX WPI; 2003-268312/26.
DR GENBANK; A29815.
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
```

PS Example 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 502 AA;

Query Match 98.1%; Score 2494; DB 7; Length 502;

Best Local Similarity 99.8%; Pred. No. 2.5e-225; Matches 478; Conservative 1; Indels 0; Gaps 0;

```
QY 3 YGTHSHGLFKKLGIGPPTPLPFLGNILSYHKGFCEMDECHKKYGVWGFYDGOQPVLA1 62
DB 24 YGTHSHGLFKKLGIGPPTPLPFLGNILSYHKGFCEMDECHKKYGVWGFYDGOQPVLA1 83
QY 63 TDPDMIKTVLVKCYSVFTNRRPFGVGFEMKSAISIAEDEMKRLRSLSPFTSGKLKE 122
DB 84 TDPDMIKTVLVKCYSVFTNRRPFGVGFEMKSAISIAEDEMKRLRSLSPFTSGKLKE 143
QY 123 MVEPIAQYGDVAVRNLRREAETGKPYTLKDVFGAYSMDVITSTSPGVNIDSLNPPDPV 182
DB 144 MVEPIAQYGDVAVRNLRREAETGKPYTLKDVFGAYSMDVITSTSPGVNIDSLNPPDPV 203
QY 183 ENTKKLRRPFLDPFLSTVFPFLPILEVANI CVPREVTNFKRSYKRMKESRLDET 242
DB 204 ENTKKLRRPFLDPFLSTVFPFLPILEVANI CVPREVTNFKRSYKRMKESRLDET 263
QY 243 OKHRVDFLOLMDSONSKETESHKALSDLELVAQSIIFIPAGYETTSVLSFIMYELATH 302
DB 264 OKHRVDFLOLMDSONSKETESHKALSDLELVAQSIIFIPAGYETTSVLSFIMYELATH 323
QY 303 PDVQOQLQOEIDAVLPNKAPPTVDVLOMEYLDVMVNETLRFPAMRLERCKKQVEIN 362
DB 324 PDVQOQLQOEIDAVLPNKAPPTVDVLOMEYLDVMVNETLRFPAMRLERCKKQVEIN 383
QY 363 GMFIPKGVVMMIPSYALHDPKWTBPEKFLPERFSKKNDIDPIYITPFGSGPRNCIG 422
DB 384 GMFIPKGVVMMIPSYALHDPKWTBPEKFLPERFSKKNDIDPIYITPFGSGPRNCIG 443
QY 423 MRFALNMKTLALIRVLQNSFPKCKETQIPLKLSLGILLQPEKPVVLKYESRDGTVSGA 481
DB 444 MRFALNMKTLALIRVLQNSFPKCKETQIPLKLSLGILLQPEKPVVLKYESRDGTVSGA 502
```

RESULT 9
AAR72363
ID AAR72363 standard; protein; 503 AA.

```

AC AAR72363;
XX
DT 25-MAR-2003 (revised)
DT 14-NOV-1995 (first entry)
XX
DE Human cytochrome P450 molecular species 3A4 protein.
XX
KW Human cytochrome P450; amplification; PCR; primer; expression vector;
KW yeast NADPH-P450 reductase; safety; fusion protein; metabolite;
KW carcinogen; mutagen; liver metabolism.
XX
OS Homo sapiens.
XX
PE EPE44267-A2.
XX
PD 22-MAR-1995.
XX
PF 20-JUL-1994; 94EP-00111298.
XX
PR 20-JUL-1993; 93JP-00201120.
PR 21-JUL-1993; 93JP-00180246.
PR 30-JUL-1993; 93JP-00208279.
XX
PA (SUMO ) SUMITOMO CHEM CO LTD.
XX
PI Hayaashi K, Sakaki T, Yabusaki Y, Komai K, Kaneko H, Nakatsuka I;
XX
DR WPI; 1995-116991/16.
DR N-PSDB; AAO87717.
XX
PT Evaluation of safety of a chemical cpd. - using recombinant yeast
XX
XX expressing human cytochrome p450 and a yeast NADPH-P450 reductase.
XX
PS Example; Page 31-33; 124pp; Eng11sh.
XX
XX The amino acid sequence of the human cytochrome P450 species 3A4. The
XX cDNA was amplified by PCR using the primers AAO87743-6. The product was
XX cloned into the yeast expression vectors PAH5N or PAHR to produce the
XX vectors p3A4 for the expression of the cytochrome P450 alone or p3A4R for
XX co-expression with the yeast NADPH-P450 reductase. The vectors are used
XX in a method for evaluating the safety of a chemical compound by reacting
XX the chemical compound with recombinantly produced human cytochrome P450
XX molecular species 1A2 (AA087714), 2C9 (AA087715), 2E1 (AA087716), or 3A4,
XX or their auxiliary species and variants (AA087718-32), and yeast NADPH-
XX P450 reductase, either as a fused protein or in cell extracts, and
XX analysing the resulting metabolite to assess the safety of the chemical
XX compound. The method is useful for determining whether the chemical
XX compound, or its metabolite, will be converted into a carcinogenic or
XX mutagenic form through metabolism in the liver. (Updated on 23-MAR-2003
XX to correct FN field.)
XX
SQ Sequence 503 AA;
XX
Query Match 98.1%; Score 2494; DB 2; Length 503;
Best Local Similarity 99.8%; Pred. No. 2.5e-225;
Matches 478; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 3 YGTHSHGLFKKLGIPPTPLPPLGNILSYHKGFCMPDMCKKXGKVGWGYDGOQPVLA1 62
DB 25 YGTHSHGLFKKLGIPPTPLPPLGNILSYHKGFCMPDMCKKXGKVGWGYDGOQPVLA1 84
QY 63 TDDPMIKTVLVKGCYSVFTNRRPFGVGFPMKSAISIADEEMKRLASLSPPTSGCKE 122
DB 85 TDDPMIKTVLVKGCYSVFTNRRPFGVGFPMKSAISIADEEMKRLASLSPPTSGCKE 144
QY 123 MVEPIAQGVNLRNLRREARLGKPVTLKDFGAYSADVTSTSGVNTISLNNPODPV 162
DB 145 MVEPIAQGVNLRNLRREARLGKPVTLKDFGAYSADVTSTSGVNTISLNNPODPV 204
QY 183 ENTKKLARPDLPDFPLSTIVFPPLPILEVLNLCVPRREVTNFKRSVKRMESRLDET 242
DB 205 ENTKKLARPDLPDFPLSTIVFPPLPILEVLNLCVPRREVTNFKRSVKRMESRLDET 264

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QY 243 QKRVDFLOQMIDSONSKETESHKALSDLELVAOSIIFIPAGYTTSSVLSFIMEIATH 302
DB 265 QKRVDFLOQMIDSONSKETESHKALSDLELVAOSIIFIPAGYTTSSVLSFIMEIATH 324
QY 303 PDVQOKQOEIDAVLPKAPPTDYTVQMEYLDVNVNETHRLPFIARLERVCCKDVEIN 362
DB 325 PDVQOKQOEIDAVLPKAPPTDYTVQMEYLDVNVNETHRLPFIARLERVCCKDVEIN 384
QY 363 GMFIPKGVVMIPSYALHRDPKWTBEKEFLPERFSKKNKNDIDPYIYTPFGSGPRNCIG 422
DB 385 GMFIPKGVVMIPSYALHRDPKWTBEKEFLPERFSKKNKNDIDPYIYTPFGSGPRNCIG 444
QY 423 MRPALNMKALIRVLONSFCKEQTQTLKLSGLLOPEKPVTLKVSBDGTSGA 481
DB 445 MRPALNMKALIRVLONSFCKEQTQTLKLSGLLOPEKPVTLKVSBDGTSGA 503

RESULT 10
AAR81464
ID AAR81464 standard; protein; 503 AA.
XX
AC AAR81464;
XX
DT 01-AUG-1996 (first entry)
XX
DE Human derived cytochrome P4503A4.
XX
KW Human derived cytochrome; P4503A4; commercial cDNA library; yeast;
KW transfection; recombinant production; expression vector; mammal;
KW immunisation; sensitisation; antibody; determination; detection;
KW non-cross reactive.
XX
OS Homo sapiens.
XX
PN JP08027197-A.
XX
PD 30-JAN-1996.
XX
PF 13-JUL-1994; 94JP-00161552.
XX
PR 13-JUL-1994; 94JP-00161552.
XX
PA (SUMO ) SUMITOMO CHEM CO LTD.
XX
PI WPI; 1996-136338/14.
XX
DR N-PSDB; AAT17399.
XX
PT Antibody recognising human derived cytochrome P4502A4 - allows specific
XX
XX detection of cytochrome P450 species in humans.
XX
PS Example 1; Page 10-12; 13pp; Japanese.
XX
XX The present sequence is the human derived cytochrome (HDC) P4503A4, which
XX was obtd. from a commercial cDNA library. Yeast was transfected with an
XX expression vector contg. the HDC cDNA, cultured and then disrupted to
XX give a microsomal fraction. The HDC was purified from the fraction, and
XX used to immunise and sensitise a mammal. Blood was drawn from the mammal,
XX CC and an anti-HDC antibody isolated. The antibody obtd. recognises HDC
XX P4503A4, partic. at a serum dilution rate of 1:10000, and is
XX substantially without cross reaction to other HDC P450 spp
XX
SQ Sequence 503 AA;
XX
Query Match 98.1%; Score 2494; DB 2; Length 503;
Best Local Similarity 99.8%; Pred. No. 2.5e-225;
Matches 478; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 3 YGTHSHGLFKKLGIPPTPLPPLGNILSYHKGFCMPDMCKKXGKVGWGYDGOQPVLA1 62
DB 25 YGTHSHGLFKKLGIPPTPLPPLGNILSYHKGFCMPDMCKKXGKVGWGYDGOQPVLA1 84
QY 63 TDDPMIKTVLVKGCYSVFTNRRPFGVGFPMKSAISIADEEMKRLASLSPPTSGCKE 122

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DB      85  TDPDMIKTVLVKECVSVFTNRRPFGVGFMKSAISIAEDDEMKRLRLSLSPFTSGKLKE 144
QY      123  MPEIIAQYGDVIVRNLRREAETGKPYTLKDVFGAYSMDVITSTSPGVNIDSLNPPDPRV 182
DB      145  MPEIIAQYGDVIVRNLRREAETGKPYTLKDVFGAYSMDVITSTSPGVNIDSLNPPDPRV 204
QY      183  ENTKKLRFDPFLDPFPLSTIVFPFLIPILEVNIICVFPREVTFPKSVKRMKESRLDET 242
DB      205  ENTKKLRFDPFLDPFPLSTIVFPFLIPILEVNIICVFPREVTFPKSVKRMKESRLDET 264
QY      243  QKRRVDFLOLMTDSQNSKETESHKALSDLELVAQSIIFIPAGYETTSVLSPIMYELATH 302
DB      265  QKRRVDFLOLMTDSQNSKETESHKALSDLELVAQSIIFIPAGYETTSVLSPIMYELATH 324
QY      303  PDVQOQLQDEIDAVLPNKAPPTDYTLQMEYLDVNNETLRPLPAMLERVCKKOVEIN 362
DB      325  PDVQOQLQDEIDAVLPNKAPPTDYTLQMEYLDVNNETLRPLPAMLERVCKKOVEIN 384
QY      363  GMFIPKGVVVMIPSYALHRDPKYTEPEKFLPERFSKKNKNDIDPIYITPFGSGPRNCIG 422
DB      385  GMFIPKGVVVMIPSYALHRDPKYTEPEKFLPERFSKKNKNDIDPIYITPFGSGPRNCIG 444
QY      423  MRPALMMKALALIRVLQNFSPFKCKETOIPLKLSLGLLQPEKPVVLKVESRDGTVSGA 481
DB      445  MRPALMMKALALIRVLQNFSPFKCKETOIPLKLSLGLLQPEKPVVLKVESRDGTVSGA 503

RESULT 11
AAR93170
ID      AAR93170 standard; protein; 503 AA.
AC      AAR93170;
XX
XX
DT      11-OCT-1996 (first entry)
XX
DE      Human cytochrome P450 molecular species 3A4 protein.
XX
KM      Human cytochrome P450; amplified; PCR; polymerase chain reaction; primer;
KM      liver; yeast; expression vector; NADPH-P450 reductase; ADH gene promoter;
KM      evaluation; safety; fusion protein; metabolite; detoxification;
KM      carcinogenic.
XX
XX      Homo sapiens.
OS
PN      JP08056695-A.
XX
PD      05-MAR-1996.
XX
PF      15-JUL-1994; 94JP-00164184.
XX
PR      20-JUL-1993; 93JP-00201120.
PR      30-JUL-1993; 93JP-00208279.
PR      17-JUN-1994; 94JP-00136053.
XX
PA      (SUMO ) SUMITOMO CHEM CO LTD.
XX
DR      WPI; 1996-182311/19.
XX
DR      N-PSDB; AAT28383.
XX
PT      Novel method for the evaluation of the safety of a cpd. - using a human
PT      cytochrome P450 and yeast NADPH reductase to determine whether the
PT      analyte cpd. is detoxified or metabolised to a carcinogen.
XX
PS      Example 1; Page 24-26; 74pp; Japanese.
XX
CC      This is the amino acid sequence of the human cytochrome P450 molecular
CC      species 3A4 protein. The corresp. gene was amplified from a human liver
CC      derived cDNA library as 2 fragments of 0.6 and 0.9 kb using primers
CC      AAT26933-6. The prod. was cloned into the yeast expression vector pAHSN
CC      to generate plasmid p3A4 for prodn. of the cytochrome only or into the
CC      vector pAHR to generate the plasmid p3A4R for co-prodn. with the yeast
CC      NADPH-P450 reductase. The sequence is placed under control of the yeast
CC      ADH gene promoter and terminator. The vectors are used in a method for
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CC      evaluating the safety of a cpd. by reacting the test cpd. with
CC      recombinantly produced human cytochrome P450 mol. species 1A2 (AAT28380),
CC      2C9 (AAT28381), 2B1 (AAT28382), 3A4 or their variants (AAT28384-98)
CC      together with yeast NADPH-P450 reductase (either as a fused protein or as
CC      a cell extract) and analysing the resultant metabolite. The cpd. is
CC      considered "safe" if it is detoxified or not rederived carcinogenic or
CC      "unsafe" if it is not detoxified or is metabolised to a carcinogenic cpd
XX
SQ      Sequence 503 AA;
Query Match      98.1%; Score 2494; DB 2; Length 503;
Best Local Similarity 99.8%; Pred. No. 2,5e-225;
Matches 478; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      3  YGTHSGLEFKKIGIEPPLPLAGNLSYHKFCFMECHKKYGVWGYGQDPVLAI 62
DB      25  YGTHSGLEFKKIGIEPPLPLAGNLSYHKFCFMECHKKYGVWGYGQDPVLAI 84
QY      63  TDPDMIKTVLVKECVSVFTNRRPFGVGFMKSAISIAEDDEMKRLRLSLSPFTSGKLKE 122
DB      85  TDPDMIKTVLVKECVSVFTNRRPFGVGFMKSAISIAEDDEMKRLRLSLSPFTSGKLKE 144
QY      123  MPEIIAQYGDVIVRNLRREAETGKPYTLKDVFGAYSMDVITSTSPGVNIDSLNPPDPRV 182
DB      145  MPEIIAQYGDVIVRNLRREAETGKPYTLKDVFGAYSMDVITSTSPGVNIDSLNPPDPRV 204
QY      183  ENTKKLRFDPFLDPFPLSTIVFPFLIPILEVNIICVFPREVTFPKSVKRMKESRLDET 242
DB      205  ENTKKLRFDPFLDPFPLSTIVFPFLIPILEVNIICVFPREVTFPKSVKRMKESRLDET 264
QY      243  QKRRVDFLOLMTDSQNSKETESHKALSDLELVAQSIIFIPAGYETTSVLSPIMYELATH 302
DB      265  QKRRVDFLOLMTDSQNSKETESHKALSDLELVAQSIIFIPAGYETTSVLSPIMYELATH 324
QY      303  PDVQOQLQDEIDAVLPNKAPPTDYTLQMEYLDVNNETLRPLPAMLERVCKKOVEIN 362
DB      325  PDVQOQLQDEIDAVLPNKAPPTDYTLQMEYLDVNNETLRPLPAMLERVCKKOVEIN 384
QY      363  GMFIPKGVVVMIPSYALHRDPKYTEPEKFLPERFSKKNKNDIDPIYITPFGSGPRNCIG 422
DB      385  GMFIPKGVVVMIPSYALHRDPKYTEPEKFLPERFSKKNKNDIDPIYITPFGSGPRNCIG 444
QY      423  MRPALMMKALALIRVLQNFSPFKCKETOIPLKLSLGLLQPEKPVVLKVESRDGTVSGA 481
DB      445  MRPALMMKALALIRVLQNFSPFKCKETOIPLKLSLGLLQPEKPVVLKVESRDGTVSGA 503

RESULT 12
AAY05202
ID      AAY05202 standard; protein; 503 AA.
XX
XX      AAY05202;
AC
XX
DT      17-JUN-1999 (first entry)
XX
DE      Human CYP3A4 protein.
XX
KM      CYP3A4 gene polymorphism; polymorphic locus; human; altered metabolism;
KM      CYP3A4 substrate; drug-drug interaction identification; toxin exposure;
KM      genetic linkage detection; phenotypic variation.
XX
OS      Homo sapiens.
XX
PN      M09913106-A1.
XX
PD      18-MAR-1999.
XX
PF      02-SEP-1998; 98WO-US018158.
XX
PR      10-SEP-1997; 97US-0058612P.
XX
PA      (AAY5-) AXXS PHARM INC.
XX
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P1 Litcher JB, Guida M;
 XX WPI: 1999-215070/18.
 DR N-PSDB; AAX28295.
 XX
 PT New isolated CYP3A4 polymorphic sequences.
 XX
 PS Disclosure; Page 25-27; 40pp; English.
 XX
 CC This sequence represents the human CYP3A4 gene protein. The invention
 CC relates to a CYP3A4 sequence polymorphism, which is part of a non-
 CC naturally occurring chromosome. Nucleic acids comprising the CYP3A4
 CC polymorphic sequences can be used to screen patients for altered
 CC metabolism for CYP3A4 substrates, potential drug-drug interactions, and
 CC adverse/side effects as well as diseases that result from environmental
 CC or occupational exposure to toxins. They can also be used to establish
 CC animal, cell culture and in vitro cell-free models for drug metabolism.
 CC Polymorphic CYP3A4 gene sequences can be used for expression studies to
 CC determine the effect of promoter and/or intron sequence variations on
 CC mRNA expression and stability. The polymorphisms are also used as single
 CC nucleotide polymorphisms to detect genetic linkage to phenotypic
 CC variation in activity and expression of CYP3A4. The nucleic acids can
 CC also be used to generate genetically modified non-human animals or site
 CC specific gene modifications in cell lines
 XX
 SQ Sequence 503 AA;

Query Match 98.1%; Score 2494; DB 2; Length 503;
 Best Local Similarity 99.8%; Pred. No. 2.5e-225;
 Matches 478; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YGTHSHGLFKKGLPGPTPLPFLGNILSYHKGFCMFMECHKKKYKMGFYDGOQPLAI 62
 DB 25 YGTHSHGLFKKGLPGPTPLPFLGNILSYHKGFCMFMECHKKKYKMGFYDGOQPLAI 84
 QY 63 TDDPMIKTVLVKCEYVFTNRPRPGVGFPMKSAISIAEDBEWRLSLSPFTSGKLXE 122
 DB 85 TDDPMIKTVLVKCEYVFTNRPRPGVGFPMKSAISIAEDBEWRLSLSPFTSGKLXE 144
 QY 123 MVEPIAQYGDVLRNLRREAEATGKPVTLKOVFGAYSMDVITSTSGVINIDSLNPPDPFV 182
 DB 145 MVEPIAQYGDVLRNLRREAEATGKPVTLKOVFGAYSMDVITSTSGVINIDSLNPPDPFV 204
 QY 183 ENTKKLRRDFLPFLPFLSTVPPFLPILLEVNICVPEPVNPLKRSYVRMKSRLSDT 242
 DB 205 ENTKKLRRDFLPFLPFLSTVPPFLPILLEVNICVPEPVNPLKRSYVRMKSRLSDT 264
 QY 243 OKHRVDFLOLMIDSQNSKETESHKALSDLEIVAQSIIFIPAGYETTSSVLSPIWELATH 302
 DB 265 OKHRVDFLOLMIDSQNSKETESHKALSDLEIVAQSIIFIPAGYETTSSVLSPIWELATH 324
 QY 303 PDVOQKLOEIBDAVLPNKAPPTVDTVLQMEYLDMMVNEILRLPFIAMRLERCKKQVEIN 362
 DB 325 PDVOQKLOEIBDAVLPNKAPPTVDTVLQMEYLDMMVNEILRLPFIAMRLERCKKQVEIN 384
 QY 363 GMFIPIKGVVMMISYALHRDPKWTBEPKFLPERFSKKNKNDIPYITYPFGSGPRNCIG 422
 DB 385 GMFIPIKGVVMMISYALHRDPKWTBEPKFLPERFSKKNKNDIPYITYPFGSGPRNCIG 444
 QY 423 MRPALMMKTLALIRVLONFSFKCKEKTQIPLKLSIGSLDPEKRVVLKVESRDGTGSA 481
 DB 445 MRPALMMKTLALIRVLONFSFKCKEKTQIPLKLSIGSLDPEKRVVLKVESRDGTGSA 503

RESULT 13
 ADQ89978
 ID ADQ89978 standard; protein: 503 AA.
 XX
 AC ADQ89978;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Antagonist of cell cycle progression polypeptide #204.

XX Cytostatic; cancer; cell division cycle; mitosis; meiosis;
 KM cell cycle progression.
 KM
 XX Homo sapiens.
 OS
 XX
 PN W02004063362-A2.
 XX
 PD 29-JUL-2004.
 XX
 PF 31-DEC-2003; 2003MO-GB005635.
 XX
 PR 10-JAN-2003; 2003JUS-0439123P.
 PR 06-MAY-2003; 2003JUS-0468402P.
 XX
 PA (CYCL-) CYCLACEL LTD.
 XX
 PI Glover D, Bell G, Frenz L, Midgley C;
 XX
 DR WPI: 2004-544089/52.
 DR N-PSDB; ADQ89977.
 XX
 PT New cell cycle progression genes and proteins for modulating cell cycle
 PT progression in cells, for preventing, treating or diagnosing cell
 PT proliferative diseases (e.g. cancer) or for identifying modulators of
 PT mitosis or meiosis.
 XX
 PS Claim 2; SEQ ID NO 408; 461pp; English.
 XX

CC The present invention relates to a polynucleotide for preventing,
 CC treating or diagnosing a disease in an individual. The composition or the
 CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
 CC diagnosing, preventing or treating diseases (e.g. cell proliferative
 CC diseases such as cancer) in an individual. These may also be used for
 CC identifying substances capable of binding to or modulating the function
 CC of the polypeptide, capable of affecting the function of the
 CC corresponding gene, or capable of inhibiting the cell division cycle or
 CC cell cycle progression, preferably mitosis and/or meiosis. The present
 CC sequence represents an antagonist of cell cycle progression protein
 CC
 CC
 XX

SQ Sequence 503 AA;

Query Match 98.1%; Score 2494; DB 8; Length 503;
 Best Local Similarity 99.8%; Pred. No. 2.5e-225;
 Matches 478; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YGTHSHGLFKKGLPGPTPLPFLGNILSYHKGFCMFMECHKKKYKMGFYDGOQPLAI 62
 DB 25 YGTHSHGLFKKGLPGPTPLPFLGNILSYHKGFCMFMECHKKKYKMGFYDGOQPLAI 84
 QY 63 TDDPMIKTVLVKCEYVFTNRPRPGVGFPMKSAISIAEDBEWRLSLSPFTSGKLXE 122
 DB 85 TDDPMIKTVLVKCEYVFTNRPRPGVGFPMKSAISIAEDBEWRLSLSPFTSGKLXE 144
 QY 123 MVEPIAQYGDVLRNLRREAEATGKPVTLKOVFGAYSMDVITSTSGVINIDSLNPPDPFV 182
 DB 145 MVEPIAQYGDVLRNLRREAEATGKPVTLKOVFGAYSMDVITSTSGVINIDSLNPPDPFV 204
 QY 183 ENTKKLRRDFLPFLPFLSTVPPFLPILLEVNICVPEPVNPLKRSYVRMKSRLSDT 242
 DB 205 ENTKKLRRDFLPFLPFLSTVPPFLPILLEVNICVPEPVNPLKRSYVRMKSRLSDT 264
 QY 243 OKHRVDFLOLMIDSQNSKETESHKALSDLEIVAQSIIFIPAGYETTSSVLSPIWELATH 302
 DB 265 OKHRVDFLOLMIDSQNSKETESHKALSDLEIVAQSIIFIPAGYETTSSVLSPIWELATH 324
 QY 303 PDVOQKLOEIBDAVLPNKAPPTVDTVLQMEYLDMMVNEILRLPFIAMRLERCKKQVEIN 362
 DB 325 PDVOQKLOEIBDAVLPNKAPPTVDTVLQMEYLDMMVNEILRLPFIAMRLERCKKQVEIN 384
 QY 363 GMFIPIKGVVMMISYALHRDPKWTBEPKFLPERFSKKNKNDIPYITYPFGSGPRNCIG 422

CC dynamics docking of one or more substrates on multi-specific enzymes.
CC Specifically, it refers to determining the three-dimensional structure of
CC active sites that are flexible and can adapt to different substrates i.e.
CC multispecific enzymes such as cytochrome P450. The present invention
CC describes identifying common structural blocks (CSBs) among members of
CC the family, aligning primary amino acid sequences, aligning the protein
CC as compared on the first alignment to obtain a second alignment, defining
CC 3D structure of protein CSBs, defining global constraints and selecting
CC rotamers, in order to determine the family of 3D model protein structures
CC and optimise models by dihedral angles. Accordingly, the method can be
CC used for screening, designing or identifying natural, unnatural or
CC substrate analogues, as well as inhibitors, activators or modulators of
CC the multispecific enzyme in question. In addition, it can determine the
CC effect of a first substrate on a second substrate, which can then be
CC applied to pharmaceutical products. Furthermore, the method can be used
CC to determine the oxidative modification of the substrate according to its
CC proximity to a haem molecule, for performing dynamic docking of the
CC metabolite either in the absence or presence of a second substrate in the
CC computed simulation and to compare the energy of the bound metabolite
CC relative to the energy of its parent substrate bound, in order to
CC determine if the exit of the given metabolite from the enzyme is favoured
CC or not. This polypeptide sequence is a protein from the cytochrome P450
CC family of enzymes, given in an exemplification of the invention.

XX
SQ Sequence 503 AA:

Query Match 96.4%; Score 2449.5; DB 8; Length 503;
Best Local Similarity 97.9%; Pred. No. 3.8e-221;
Matches 470; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 3 YGTHSHGLFKKLGIPGTPPLPLIGNILSYHKGFCMFMECHKKYGKMGFYDGOQPYLAI 62
DB 24 YGTHSHGLFKKLGIPGTPPLPLIGNILSYHKGFCMFMECHKKYGKMGFYDGOQPYLAI 83
QY 63 TDDPMIKTVLVKECYSVFTNRPRPGVGFMSAISIADEEWKRLRSLSPFTSGKLKE 122
DB 84 TDDPMIKTVLVKECYSVFTNRPRPGVGFMSAISIADEEWKRLRSLSPFTSGKLKE 143
QY 123 MVLPIAQYGVLVNRLRREAEKGVTLKDVFGAYSMDVITSTSGVNIIDSLNPDPEV 182
DB 144 MVLPIAQYGVLVNRLRREAEKGVTLKDVFGAYSMDVITSTSGVNIIDSLNPDPEV 203
QY 183 ENTKKLRFPDLDFPFLSTIVPPLPILEVLNLCVPRREVTNFKSVRMKESRLDET 242
DB 204 ENTKKLRFPDLDFPFLSTIVPPLPILEVLNLCVPRREVTNFKRAVVRMKESRLDET 263
QY 243 QKRRVDFLQMLIDS-QNSKETESHKALSDLELVAQSIIFIPAGYETTSVLSFIMYELAT 301
DB 264 QKRRVDFLQMLIDSQNSKETESHKALSDLELVAQSIIFIPAGYETTSVLSFIMYELAT 323
QY 302 HPDVQOKLQBEIDAVALPNKAPPTYDVVLQMEYLDVNVNETHRLPLIAMRLERVCCKDVEI 361
DB 324 HPDVQOKLQBEIDAVALPNKAPPTYDVVLQMEYLDVNVNETHRLPLIAMRLERVCCKDVEI 383
QY 362 NGMFIPKGVVVMPSYALHDDPKWTEPEKFLPERFSKKNKNDIPYITPFGSGPRNCI 421
DB 384 NGMFIPKGVVVMPSYALHDDPKWTEPEKFLPERFSKKNKNDIPYITPFGSGPRNCI 443
QY 422 GMRFALNMMLALIRVLQNSFKPKCKETOIPLKLSLGGILOPEKPVVLKYESRDGTVSGA 481
DB 444 GMRFALNMMLALIRVLQNSFKPKCKETOIPLKLSLGGILOPEKPVVLKYESRDGTVSGA 503

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Job time : 171 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2005, 14:10:22 ; Search time 41 Seconds

(without alignments)
1138.174 Million cell updates/sec

Title: US-10-690-991-2

Perfect score: 2542
Sequence: 1 MAYGTHSHGLPKLGIKIRPT.....PVLAKVSRDGTSGAHHH 485

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2501	98.4	503	2	A29815
2	2449.5	96.4	504	2	A29410
3	2372	93.3	503	2	S28168
4	2233	87.8	503	2	JX0062
5	2142.5	84.3	502	1	A34101
6	2077	81.7	503	2	SI4275
7	2003	78.8	503	2	UC4702
8	1989	78.2	501	2	A34206
9	1961	77.1	503	2	S50211
10	1957	77.0	503	2	JC7627
11	1946.5	76.6	504	2	A22631
12	1937	76.2	501	2	A29487
13	1935.5	76.1	504	2	A60564
14	1904.5	74.9	502	2	A25222
15	1902.5	74.8	504	2	JX0334
16	1878.5	73.9	504	2	S50892
17	1802	70.9	497	2	S52097
18	1788	70.3	503	2	A40843
19	838.5	33.0	534	2	A41766
20	837.5	32.9	533	1	S448161
21	827.5	32.6	533	2	S42404
22	789.5	31.1	533	2	JN0683
23	656.5	25.8	460	2	B41766
24	656	25.8	509	1	A32157
25	639	25.1	518	2	T24783
26	630	24.8	518	2	T20908
27	626	24.6	498	1	S48058
28	623	24.5	520	2	T24777
29	621.5	24.4	507	1	A47198

30	620.5	24.4	519	2	T24784	hypothetical prote
31	602.5	23.7	509	2	T24785	hypothetical prote
32	599	23.6	517	2	T20907	hypothetical prote
33	595.5	23.4	503	2	JC5321	cytochrome P450 mo
34	594	23.4	520	2	T24778	hypothetical prote
35	591.5	23.3	518	2	T24779	hypothetical prote
36	590.5	23.2	510	2	T19763	hypothetical prote
37	588.5	23.2	522	2	T19762	hypothetical prote
38	587	23.1	520	2	T24780	hypothetical prote
39	556.5	21.9	515	2	T24781	hypothetical prote
40	543.5	21.4	496	1	S41192	cytochrome P450 4D
41	530.5	20.9	513	2	JC7120	cytochrome P450 en
42	529	20.8	494	2	JC5320	cytochrome P450 mo
43	528.5	20.8	544	2	T27750	hypothetical prote
44	520.5	20.5	501	2	T19766	hypothetical prote
45	520	20.5	475	2	A88414	protein C36A4.3 [1

ALIGNMENTS

RESULT 1
A29815
Cytochrome P450 3A4 nifedipine oxidase (EC 1.14.14.-) - human
N:Alternate names: cytochrome P450(PCN1); cytochrome P450-HM1
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1989 #sequence revision 30-Sep-1989 #text change 09-Jul-2004
C:Accession: A29815; S16900; A25517; A32199; PX0012; S03851
R:Gonzalez, F.J.; Schmid, B.J.; Umeno, M.; McBride, O.W.; Hardwick, J.P.; Meyer, U.A.;
DNA 7, 79-86, 1988
A:Title: Human P450PCN1: sequence, chromosome localization, and direct evidence through
A:Reference number: A29815; MUID:88195781; PMID:3267210
A:Accession: A29815
A:Molecule type: mRNA
A:Residues: 1-503 <CON>
A:Cross-references: UNIROR:P08684; GB:M18907; NID:G181373; PIDN:AAA5745.1; PID:G18137
R:Spurr, N.K.; Gough, A.C.; Stevenson, K.; Wolf, C.R.
Hum. Genet. 81, 171-174, 1989
A:Title: The human cytochrome P450 CYP3 locus: assignment to chromosome 7q22-qter.
A:Reference number: S16900; MUID:89108438; PMID:2563251
A:Accession: S16900
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-391, 'W', 393-503 <SP2>
A:Cross-references: EMBL:X12387; NID:G35910; PIDN:CA30944.1; PID:G35911
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1988
R:Beaune, P.H.; Umbenhauer, D.R.; Bork, R.W.; Lloyd, R.S.; Guengerich, F.P.
Proc. Natl. Acad. Sci. U.S.A. 83, 8064-8068, 1986
A:Title: Isolation and sequence determination of a cDNA clone related to human cytochro
A:Reference number: A25517; MUID:87041402; PMID:3464943
A:Accession: A25517
A:Molecule type: mRNA
A:Residues: 1-391, 'W', 393-503 <BEA>
R:Bork, R.W.; Muto, T.; Beaune, P.H.; Srivastava, P.K.; Lloyd, R.S.; Guengerich, F.P.
J. Biol. Chem. 264, 910-919, 1989
A:Title: Characterization of mRNA species related to human liver cytochrome P-450 nifed
A:Reference number: A32199; MUID:89093163; PMID:2463251
A:Accession: A32199
A:Molecule type: protein
A:Residues: 'X', 2-9, 'XXX', 13-15 <BOR>
R:Komori, M.; Hashizume, T.; Ohi, H.; Mura, T.; Kitada, M.; Nagashima, K.; Kametaki, T
J. Biochem. 104, 912-916, 1988
A:Title: Cytochrome P-450 in human liver microsomes: high-performance liquid chromatogr
A:Reference number: PX0012; MUID:89214010; PMID:3243766
A:Accession: PX0012
A:Molecule type: protein
A:Residues: 'X', 2-11, 'X', 13-25 <KOM>
A:Experimental source: liver microsomes
C:Genetics:
A:Gene: GDB:CYP3A4
A:Cross-references: GDB:118782
A:Map position: 7q22.1-7q22.1
C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology

C/keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metallo
F:302-464/Domain: cytochrome P450 homology <P45>
F:442/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 98.4%; Score 2501; DB 2; Length 503;
Best Local Similarity 100.0%; Pred. No. 3.6e-179;
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 YGTHSHGLFKKGIIPGPPLPFLGNILSYHKFCMFDECHKYKGVNGFYDGOQPVLA 62
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DB 25 YGTHSHGLFKKGIIPGPPLPFLGNILSYHKFCMFDECHKYKGVNGFYDGOQPVLA 84
    |||||
QY 63 TDPDMIKTVLVKCYSVFTNRRPFGVGFPMKSAISIADEEMKRLRLSLPFTSGKKE 122
    |||||
DB 85 TDPDMIKTVLVKCYSVFTNRRPFGVGFPMKSAISIADEEMKRLRLSLPFTSGKKE 144
    |||||
QY 123 MPEIIAQGDVAVRNLRREARETGKPYTLKDVFGAYSMDVITSTSGVNIIDSLNPODPV 182
    |||||
DB 145 MPEIIAQGDVAVRNLRREARETGKPYTLKDVFGAYSMDVITSTSGVNIIDSLNPODPV 204
    |||||
QY 183 ENTKKLRLDFDLPFLSTIVPEPLPILEVNICVFPREVNFARKSVKMKESRLBPT 242
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DB 205 ENTKKLRLDFDLPFLSTIVPEPLPILEVNICVFPREVNFARKSVKMKESRLBPT 264
    |||||
QY 243 QKRVDFLOLMIDSQNSKETESHKALSDLELVAOSIIFIFAGYETTSSVLSFIMYELAT 302
    |||||
DB 265 QKRVDFLOLMIDSQNSKETESHKALSDLELVAOSIIFIFAGYETTSSVLSFIMYELAT 324
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QY 303 PDVQOQKQEEIDAVLPNKAPPTVDYVLOMEYLDVNVNELLRLPFLAMLERVCKKDV 362
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DB 325 PDVQOQKQEEIDAVLPNKAPPTVDYVLOMEYLDVNVNELLRLPFLAMLERVCKKDV 384
    |||||
QY 363 GMFIPKGVVMIIPSYALHDPKWTPEPEKFLPERFSKKNKNDIPYITPFGSGPRNCTG 422
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DB 385 GMFIPKGVVMIIPSYALHDPKWTPEPEKFLPERFSKKNKNDIPYITPFGSGPRNCTG 444
    |||||
QY 423 MRPALMMKALIRVLONFSEFKCKEQTQIPKLKSLGGLQPEKPVVLKVESRDGTVSGA 481
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DB 445 MRPALMMKALIRVLONFSEFKCKEQTQIPKLKSLGGLQPEKPVVLKVESRDGTVSGA 503
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RESULT 2

A29410
Cytochrome P450, glucocorticoid-inducible, hepatic - human
N/alternate names: cytochrome P450 3A3; cytochrome P450 HLP
N/contams: oxidoreductase (EC 1.-.-.-)

C/Species: Homo sapiens (man)
C/Date: 31-Mar-1989 #sequence, revision 31-Mar-1989 #text_change 09-Jul-2004

C/Accession: A29410; A25170; A25450

R:MoIowa, D.T.; Schuetz, E.G.; Wrighton, S.A.; Watkins, P.B.; Kremers, P.; Mendez-Picon, Proc. Natl. Acad. Sci. U.S.A. 83, 5311-5315, 1986

A/Title: Complete cDNA sequence of a cytochrome P-450 inducible by glucocorticoids in hu
A/Reference number: A94111; MUID:86259780; PMID:3460094

A/Accession: A29410

A/Molecule type: mRNA

A/Residues: 1-504 <MOL>

A/Cross-references: UNIPROT:P05184; GB:M13785; NID:g181353; PIDN:AA35742.1; PID:g181354

R:Watkins, P.B.; Wrighton, S.A.; Maurel, P.; Schuetz, E.G.; Mendez-Picon, G.; Parker, G. Proc. Natl. Acad. Sci. U.S.A. 82, 6310-6314, 1985

A/Title: Identification of an inducible form of cytochrome P-450 in human liver.
A/Reference number: A25170; MUID:85298342; PMID:3898085

A/Accession: A25170

A/Molecule type: protein

A/Residues: 2-21 <MAT>

C/Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology

C/Keywords: chromoprotein; electron transfer; heme; iron; liver; metalloprotein; monooxy

F:303-465/Domain: cytochrome P450 homology <P45>

F:442/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 96.4%; Score 2449.5; DB 2; Length 504;
Best Local Similarity 97.9%; Pred. No. 2.6e-175;
Matches 470; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

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QY 3 YGTHSHGLFKKGIIPGPPLPFLGNILSYHKFCMFDECHKYKGVNGFYDGOQPVLA 62
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DB 25 YGTHSHGLFKKGIIPGPPLPFLGNILSYHKFCMFDECHKYKGVNGFYDGOQPVLA 84
    |||||
QY 63 TDPDMIKTVLVKCYSVFTNRRPFGVGFPMKSAISIADEEMKRLRLSLPFTSGKKE 122
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DB 85 TDPDMIKTVLVKCYSVFTNRRPFGVGFPMKSAISIADEEMKRLRLSLPFTSGKKE 144
    |||||
QY 123 MPEIIAQGDVAVRNLRREARETGKPYTLKDVFGAYSMDVITSTSGVNIIDSLNPODPV 182
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DB 145 MPEIIAQGDVAVRNLRREARETGKPYTLKDVFGAYSMDVITSTSGVNIIDSLNPODPV 204
    |||||
QY 183 ENTKKLRLDFDLPFLSTIVPEPLPILEVNICVFPREVNFARKSVKMKESRLBPT 242
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DB 205 ENTKKLRLDFDLPFLSTIVPEPLPILEVNICVFPREVNFARKSVKMKESRLBPT 264
    |||||
QY 243 QKRVDFLOLMIDSQNSKETESHKALSDLELVAOSIIFIFAGYETTSSVLSFIMYELAT 301
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DB 265 QKRVDFLOLMIDSQNSKETESHKALSDLELVAOSIIFIFAGYETTSSVLSFIMYELAT 324
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QY 303 PDVQOQKQEEIDAVLPNKAPPTVDYVLOMEYLDVNVNELLRLPFLAMLERVCKKDV 361
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DB 325 PDVQOQKQEEIDAVLPNKAPPTVDYVLOMEYLDVNVNELLRLPFLAMLERVCKKDV 384
    |||||
QY 363 GMFIPKGVVMIIPSYALHDPKWTPEPEKFLPERFSKKNKNDIPYITPFGSGPRNCT 421
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DB 385 GMFIPKGVVMIIPSYALHDPKWTPEPEKFLPERFSKKNKNDIPYITPFGSGPRNCT 444
    |||||
QY 423 MRPALMMKALIRVLONFSEFKCKEQTQIPKLKSLGGLQPEKPVVLKVESRDGTVSGA 481
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DB 445 MRPALMMKALIRVLONFSEFKCKEQTQIPKLKSLGGLQPEKPVVLKVESRDGTVSGA 504
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RESULT 3

S28168
Nifedipine oxidase (EC 1.14.14.-) cytochrome P450 3A8 - crab-eating macaque
N/alternate names: cytochrome P450 CMC; cytochrome P450 Mnf2; cytochrome P450-MK2
C/Species: Macaca fascicularis (crab-eating macaque)

C/Date: 28-May-1993 #sequence, revision 28-May-1993 #text_change 09-Jul-2004

C/Accession: S28168; S04509; S36875

R:Komori, M.; Kikuchi, O.; Sakuma, T.; Funaki, T.; Kitada, M.; Kametaki, T. Biochim. Biophys. Acta 1171, 141-146, 1992

A/Title: Molecular cloning of monkey liver cytochrome P-450 cDNAs: similarity of the pri

A/Reference number: S28168; MUID:93129612; PMID:1282830

A/Accession: S28168

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-503 <KOM>

A/Cross-references: UNIPROT:P33268; GB:S53047; NID:g263692; PIDN:AA24952.1; PID:g263693

R:Ohita, K.; Kitada, M.; Hashizume, T.; Komori, M.; Ohi, H.; Kametaki, T. Biochim. Biophys. Acta 996, 142-145, 1989

A/Title: Purification of cytochrome P-450 from polychlorinated biphenyl-treated crab-eat
A/Reference number: S04509; MUID:89287352; PMID:2500151

A/Accession: S04509

A/Molecule type: protein

A/Residues: 1-22 <OHT>

R:Ohmori, S.; Horie, T.; Guengerich, F.P.; Kikuchi, M.; Kitada, M. Arch. Biochem. Biophys. 305, 405-413, 1993

A/Title: Purification and characterization of two forms of hepatic microsomal cytochrome

A/Reference number: S36874; MUID:93384294; PMID:8373178

A/Accession: S36875

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-13 <OHM>

C/Genetics: CYP3A8

C/Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology

C/Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metallo

F:302-464/Domain: cytochrome P450 homology <P45>

F:442/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 93.3%; Score 2372; DB 2; Length 503;
Best Local Similarity 93.9%; Pred. No. 1.6e-169;

Matches 450; Conservative 18; Mismatches 11; Indels 0; Gaps 0;

QY 3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGCMPMECHKYKXKXWGPFDGQPLAI 62
 DB 25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFTEFMCECKYKXKXWGPFDGQPLAI 84
 QY 63 TDPDMIKTVLVKCECVFTNRPRPGVGFPMKSAISIADEBEWKRLSLSPFTSGKLKE 122
 DB 85 TDPDMIKTVLVKCECVFTNRPRPGVGFPMKSAISIADEBEWKRLSLSPFTSGKLKE 144
 QY 123 MVLPIAOGDVLVRLNLRREAEKGPVTLKDFGAYSMGVITSTSPGVNIDSLNPPDPFV 182
 DB 145 MVLPIAOGDVLVRLNLRREAEKGPVTLKDFGAYSMGVITSTSPGVNIDSLNPPDPFV 204
 QY 183 ENTKKLRFDLPFLPFLSTIVFPFLIPILEVNI CVPPREVTNPLKSKYKMKESRLDET 242
 DB 205 ENTKKLRFDLPFLPFLSTIVFPFLIPILEVNI CVPPREVTNPLKSKYKMKESRLDET 264
 QY 243 QKRVDPLQMLDMSQSKETESHKALSDLELVAOSIIFIPAGYETTSVLSFIYELATH 302
 DB 265 QKRVDPLQMLDMSQSKETESHKALSDLELVAOSIIFIPAGYETTSVLSFIYELATH 324
 QY 303 PDVQOKLOEIDAVLPNKAPPTVDVLOMEYLDVNVNLTLPFLIARLERVCKKQVEIN 362
 DB 325 PDVQOKLOEIDAVLPNKAPPTVDVLOMEYLDVNVNLTLPFLIARLERVCKKQVEIN 384
 QY 363 GMFIPKGVVMIPISYALHDPKWTBPEKFLPERFSKXKXNDIDPIYTPFGSGPRNCIG 422
 DB 385 GMFIPKGVVMIPISYALHDPKWTBPEKFLPERFSKXKXNDIDPIYTPFGSGPRNCIG 444
 QY 423 MRPALNMKALIRVLQNSFPKCKETOIPLKLSLGLLOPEKPVVLKVSRLDGTVSGA 481
 DB 445 MRPALNMKALIRVLQNSFPKCKETOIPLKLSLGLLOPEKPVVLKVSRLDGTVSGA 503

RESULT 4

JX0062
 N/Alternate names: cytochrome P450 3A7 - human
 N/Contains: oxidoreductase (EC 1.-.-.-)
 C/Species: Homo sapiens (man)
 C/Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 09-Jul-2004
 C/Accession: JX0062; PX0014; S04983; S02152
 R/Komori, M.; Nishio, K.; Ohl, H.; Kikada, M.; Kametaki, T.
 J. Biochem. 105, 161-163, 1989
 A/Title: Molecular cloning and sequence analysis of cDNA containing the entire coding re
 A/Reference number: JX0062; MUID:8925154; PMID:2722762
 A/Accession: JX0062
 A/Molecule type: mRNA
 A/Residues: 1-503 <KOM>
 A/Cross-references: UNIPROT:P24463; GB:D00408; NID:g220148; PIDN:BA00310.1; PID:g220149
 A/Experimental source: fetal liver
 R/Komori, M.; Hashizume, T.; Ohl, H.; Miura, T.; Kikada, M.; Nagashima, K.; Kametaki, T.
 J. Biochem. 104, 912-916, 1988
 A/Title: Cytochrome P-450 in human liver microsomes: high-performance liquid chromatogra
 A/Reference number: PX0012; MUID:89214010; PMID:3243766
 A/Accession: PX0014
 A/Molecule type: protein
 A/Residues: 1-25 <KO2>
 A/Experimental source: liver microsomes
 R/Komori, M.; Nishio, K.; Fujitani, T.; Ohl, H.; Kikada, M.; Miura, S.; Itahashi, K.; Kam
 Arch. Biochem. Biophys. 272, 219-225, 1989
 A/Title: Isolation of a new human fetal liver cytochrome P450 cDNA clone: evidence for e
 A/Reference number: S04983; MUID:89286124; PMID:2786707
 A/Accession: S04983
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 282-503 <KO3>
 R/Wrighton, S.A.; VandenBranden, M.
 Arch. Biochem. Biophys. 268, 144-151, 1989
 A/Title: Isolation and characterization of human fetal liver cytochrome P450H1p2: a chi
 A/Reference number: S02152; MUID:89104413; PMID:2492179
 A/Accession: S02152

A/Molecule type: protein
 A/Residues: 1-11, 'X', 13-25, 'X', 27-30 <WRI>
 A/Genetics:
 A/Gene: GDB:CYP3A7
 A/Cross-references: GDB:134409
 A/Map position: 7q22.1-7q22.1
 C/Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
 C/Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metallo
 F/302-664/domain: cytochrome P450 homology <P45>
 F/442/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match

87.8%; Score 2233; DB 2; Length 503;
 Best Local Similarity 88.7%; Pred. No. 3, 9e-159;

Matches 425; Conservative 27; Mismatches 27; Indels 0; Gaps 0;

QY 3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGCMPMECHKYKXKXWGPFDGQPLAI 62
 DB 25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFTEFMCECKYKXKXWGPFDGQPLAI 84
 QY 63 TDPDMIKTVLVKCECVFTNRPRPGVGFPMKSAISIADEBEWKRLSLSPFTSGKLKE 122
 DB 85 TDPDMIKTVLVKCECVFTNRPRPGVGFPMKSAISIADEBEWKRLSLSPFTSGKLKE 144
 QY 123 MVLPIAOGDVLVRLNLRREAEKGPVTLKDFGAYSMGVITSTSPGVNIDSLNPPDPFV 182
 DB 145 MVLPIAOGDVLVRLNLRREAEKGPVTLKDFGAYSMGVITSTSPGVNIDSLNPPDPFV 204
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 DB 205 ENTKKLRFDLPFLPFLSTIVFPFLIPILEVNI CVPPREVTNPLKSKYKMKESRLDET 264
 QY 243 QKRVDPLQMLDMSQSKETESHKALSDLELVAOSIIFIPAGYETTSVLSFIYELATH 302
 DB 265 QKRVDPLQMLDMSQSKETESHKALSDLELVAOSIIFIPAGYETTSVLSFIYELATH 324
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 DB 325 PDVQOKLOEIDAVLPNKAPPTVDVLOMEYLDVNVNLTLPFLIARLERVCKKQVEIN 384
 QY 363 GMFIPKGVVMIPISYALHDPKWTBPEKFLPERFSKXKXNDIDPIYTPFGSGPRNCIG 422
 DB 385 GMFIPKGVVMIPISYALHDPKWTBPEKFLPERFSKXKXNDIDPIYTPFGSGPRNCIG 444
 QY 423 MRPALNMKALIRVLQNSFPKCKETOIPLKLSLGLLOPEKPVVLKVSRLDGTVSGA 481
 DB 445 MRPALNMKALIRVLQNSFPKCKETOIPLKLSLGLLOPEKPVVLKVSRLDGTVSGA 503

RESULT 5

A34101
 N/Alternate names: cytochrome P450 3A5 - human
 N/Contains: oxidoreductase (EC 1.-.-.-)
 C/Species: Homo sapiens (man)
 C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: A34101; S06491; I52302
 R/Aoyama, T.; Yamano, S.; Waxman, D.J.; Lapidson, D.P.; Meyer, U.A.; Fischer, V.; Tyndal
 J. Biol. Chem. 264, 10388-10395, 1989
 A/Title: Cytochrome P-450 hPCN3, a novel cytochrome P-450 IITa gene product that is dif
 DNA-expressed hPCN1 and hPCN3 for the metabolism of steroid hormones and cyclosporine.
 A/Reference number: A34101; MUID:89278055; PMID:2732228
 A/Accession: A34101
 A/Molecule type: mRNA
 A/Residues: 1-502 <AOY>
 A/Cross-references: UNIPROT:P20815; GB:J04813; NID:g181345; PIDN:AAA02993.1; PID:g181346
 R/Schuetz, J.D.; Molowa, D.T.; Guzelian, P.S.
 Arch. Biochem. Biophys. 274, 355-365, 1989
 A/Title: Characterization of a cDNA encoding a new member of the glucocorticoid-response
 A/Reference number: S06491; MUID:90025114; PMID:2802615
 A/Accession: S06491
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-304, 'P', 306-317, 'F', 319-323, 'D', 325-376, 'G', 378-502 <SCH>

R:Jounaidi, Y.; Guzelian, P.S.; Maurel, P.; Villarem, M.J.

Biochem. Biophys. Res. Commun. 205, 1741-1747, 1994

A:Title: Sequence of the 5'-flanking region of CYP3A5: comparative analysis with CYP3A4

A:Reference number: 152302; MUID:95110318; PMID:7811260

A:Accession: 152302

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-24 <RES>

A:Cross-references: GB:S74699; NID:G786472; PIDN:AAD14157.1; PID:G4261857

C:Genetics:

A:Gene: CYP3A5

A:Cross-references: GDB:118783

A:Map position: 7q22.1-7q22.1

C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology

C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase; F/302-464/Domain: cytochrome P450 homology <P45>

F/441/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 84.3%; Score 2142.5; DB 1; Length 502;

Best Local Similarity 84.1%; Pred. No. 2.3e-152;

Matches 402; Conservative 37; Mismatches 38; Indels 1; Gaps 1;

3 YGTHSHGLFKKLGIPPTPLPFLGNILSYHGFCEMDECHKKYKVGWGFYDGOQPVLA1 62

25 YGTRTHGLFKRLGIPPTPLPFLGNILSYHGFCEMDECHKKYKVGWGFYDGOQPVLA1 84

63 TDPDMIKTVLVKCYSVFTNRRPFGVGFMSKSAISAEDEWKRRLSLSPFTSGKLKE 122

85 TDPDVIKTVLVKCYSVFTNRRPFGVGFMSKSAISAEDEWKRRLSLSPFTSGKLKE 144

123 MPTIIQYGVDLVNNLRREAEKGPVTLKDFGAYSMVDITSTSGVNIIDSLNPDPPV 182

145 MPTIIQYGVDLVNNLRREAEKGPVTLKDFGAYSMVDITSTSGVNIIDSLNPDPPV 204

183 ENTKKLRLPDLPPFLSITVPPELIPLEVLNLCVFPREVTNPLKSKYKMKESRLBDT 242

205 ESTKKLRLPDLPPFLSITVPPELIPLEVLNLCVFPREVTNPLKSKYKMKESRLBDT 264

243 QGRVDFLOLMIDSONSKETESHKALSDLEVAOSIIFPAGYETTSVLSFTMYELATH 302

265 QGRVDFLOLMIDSONSKETESHKALSDLEVAOSIIFPAGYETTSVLSFTMYELATH 324

303 PDVQOKLOEIDAVLPNKAPPTVDVLOMEYLDVNNETLRLEPIAMRLERYCKKQVEIN 362

325 PDVQOKLOEIDAVLPNKAPPTVDVLOMEYLDVNNETLRLEPIAMRLERYCKKQVEIN 384

363 GMFIPKGVVMMIPSYALHRDPKWTPEKFLPERFSKKNKNDIPYITTFPGSGPRNCIG 422

385 GMFIPKGVVMMIPSYALHRDPKWTPEKFLPERFSKKNKNDIPYITTFPGSGPRNCIG 443

423 MRPALMMKALIRVLQNFSPFKCKETOIPLKLSLGLLOPEKPVVLKVESRDGTVSG 480

444 MRPALMMKALIRVLQNFSPFKCKETOIPLKLSLGLLOPEKPVVLKVESRDGTVSG 501

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

C:Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metallo

F/302-464/Domain: cytochrome P450 homology <P45>

F/442/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 81.7%; Score 2077; DB 2; Length 503;

Best Local Similarity 79.7%; Pred. No. 1.8e-147;

Matches 382; Conservative 55; Mismatches 42; Indels 0; Gaps 0;

3 YGTHSHGLFKKLGIPPTPLPFLGNILSYHGFCEMDECHKKYKVGWGFYDGOQPVLA1 62

25 YGTRTHGLFKRLGIPPTPLPFLGNILSYHGFCEMDECHKKYKVGWGFYDGOQPVLA1 84

63 TDPDMIKTVLVKCYSVFTNRRPFGVGFMSKSAISAEDEWKRRLSLSPFTSGKLKE 122

85 TDPDVIKTVLVKCYSVFTNRRPFGVGFMSKSAISAEDEWKRRLSLSPFTSGKLKE 144

123 MPTIIQYGVDLVNNLRREAEKGPVTLKDFGAYSMVDITSTSGVNIIDSLNPDPPV 182

145 MPTIIQYGVDLVNNLRREAEKGPVTLKDFGAYSMVDITSTSGVNIIDSLNPDPPV 204

183 ENTKKLRLPDLPPFLSITVPPELIPLEVLNLCVFPREVTNPLKSKYKMKESRLBDT 242

205 ESTKKLRLPDLPPFLSITVPPELIPLEVLNLCVFPREVTNPLKSKYKMKESRLBDT 264

243 QGRVDFLOLMIDSONSKETESHKALSDLEVAOSIIFPAGYETTSVLSFTMYELATH 302

265 QGRVDFLOLMIDSONSKETESHKALSDLEVAOSIIFPAGYETTSVLSFTMYELATH 324

303 PDVQOKLOEIDAVLPNKAPPTVDVLOMEYLDVNNETLRLEPIAMRLERYCKKQVEIN 362

325 PDVQOKLOEIDAVLPNKAPPTVDVLOMEYLDVNNETLRLEPIAMRLERYCKKQVEIN 384

363 GMFIPKGVVMMIPSYALHRDPKWTPEKFLPERFSKKNKNDIPYITTFPGSGPRNCIG 422

385 GMFIPKGVVMMIPSYALHRDPKWTPEKFLPERFSKKNKNDIPYITTFPGSGPRNCIG 444

423 MRPALMMKALIRVLQNFSPFKCKETOIPLKLSLGLLOPEKPVVLKVESRDGTVSG 481

445 MRPALMMKALIRVLQNFSPFKCKETOIPLKLSLGLLOPEKPVVLKVESRDGTVSG 503

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

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Qy

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Qy

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Qy

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Qy

Db

Qy

Db

Qy

Db

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Db 85 TDPDIKIVLVKECSTFNRRNPGVGLIKKALISIDSEKRIIRALLSPFTSGKAKE 144
Qy 123 MWPPIAAGDVLVNRNLRREAEATGKVTLLKDFGAYSMVITSTSGVNIIDSLNPPQDFV 182
Db 145 MPPINQYTDMLVNRMRQSGSEKPTSMKDIIFGAYSMVITATSGVNVDSINNPDQDFV 204
Qy 183 ENTKKLARFDLDPFLPSITVPFPLIPLEVLNLCVFPREVTNPLRKSVMKESRLDET 242
Db 205 EKVKKLLKFDLPFLPSITVPFPLIPLEVLNLCVFPREVTNPLRKSVMKESRLDET 264
Qy 243 QKRVDFLOLMIDSONSKETESHKALSDLEVAQSIIFIPAGYETTSVLSFIMYELATH 302
Db 265 EKQWMDPFLQMINSGNSKVSHKSLSDVEIVAQSVITIPAGYETTSVLSFVLYLAIH 324
Qy 303 PDVQOKLOEIDAVLPNKAPPTVDTVLQMEYLDVNVNELLRLPPIAMLERVCKKQVEIN 362
Db 325 PDIOKKQDEIDALPNKAAHYDTLLQMEYLDVNVNELLRLPPIAGLERVCKQVEIN 384
Qy 363 GMPIPKGVVMMIPSYALHRDPKWTBEPKFLPERFSKKNQNDIPYITPPGSGPRNCTG 422
Db 385 GVPIPKGVVMMIPFALHDPKWTBEPKFLPERFSKKNQNDIPYITPPGSGPRNCTG 444
Qy 423 MRPALMMKALIRVLQNFSPKCKETQIPKLKSLGGLQPEKPVVLKVESRDGTVSGA 481
Db 445 MRPALMMKALIRVLQNFSPKCKETQIPKLKSLGGLQPEKPVVLKVESRDGTVSGA 503
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RESULT 8

A34236
cytochrome P450 3A6 (version 2) - rabbit
N/Alternate names: cytochrome P450 3c
N/Contains: oxidoreductase (EC 1.-.-.-)
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 31-May-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: A34236
R/Potenza, C.L.; Pendurthi, U.R.; Strom, D.K.; Tukey, R.H.; Griffin, K.J.; Schwab, G.B.;
J. Biol. Chem. 264, 16222-16228, 1989
A/Title: Regulation of the rabbit cytochrome P-450 3c gene. Age-dependent expression and
A/Reference number: A34236; MUID:89380226; PMID:277787
A/Molecule type: mRNA
A/Residues: 1-501 <PDB>
A/Cross-references: UNIPROT:P11707; GB:J05034; NID:G164829; PIDN:AAA31178.1; PID:G164830
C/Genetic8:
A/Gene: CYP3A6
C/Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C/Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F/302-462/Domain: cytochrome P450 homology <P45>
F/440/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 78.2%; Score 1989; DB 2; Length 501;
Best Local Similarity 76.0%; Pred. No. 6,9e-141;
Matches 364; Conservative 64; Mismatches 51; Indels 0; Gaps 0;

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Qy 3 YGTHSHGLFKKLGIPGTPPLPFLGNILSYHKGFCMPMECHKKYGKVMGFYDGOQVLA 62
Db 23 YGTHSHGLFKKLGIPGTPPLPFLGNILSYHKGFCMPMECHKKYGKVMGFYDGOQVLA 82
Qy 63 TDPDMIKTVLVKECYSFTRRRRPGVPYFPMKSAISIADEEMKRLRLSLPTFTSGKAKE 122
Db 83 TDPDMIKTVLVKECYSFTRRRRPGVPYFPMKSAISIADEEMKRLRLSLPTFTSGKAKE 142
Qy 123 MWPPIAAGDVLVNRNLRREAEATGKVTLLKDFGAYSMVITSTSGVNIIDSLNPPQDFV 182
Db 143 MWPPIAAGDVLVNRNLRREAEATGKVTLLKDFGAYSMVITSTSGVNIIDSLNPPQDFV 202
Qy 183 ENTKKLARFDLDPFLPSITVPFPLIPLEVLNLCVFPREVTNPLRKSVMKESRLDET 242
Db 203 ENTKKLARFDLDPFLPSITVPFPLIPLEVLNLCVFPREVTNPLRKSVMKESRLDET 262
Qy 243 QKRVDFLOLMIDSONSKETESHKALSDLEVAQSIIFIPAGYETTSVLSFIMYELATH 302
Db 263 QKRVDFLOLMIDSONSKETESHKALSDLEVAQSIIFIPAGYETTSVLSFIMYELATH 322
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Db 263 QKRVDFLOLMIDSONSKETESHKALSDLEVAQSIIFIPAGYETTSVLSFIMYELATH 322
Qy 303 PDVQOKLOEIDAVLPNKAPPTVDTVLQMEYLDVNVNELLRLPPIAMLERVCKKQVEIN 362
Db 323 PDVQOKLOEIDAVLPNKAPPTVDTVLQMEYLDVNVNELLRLPPIAMLERVCKKQVEIN 382
Qy 363 GMPIPKGVVMMIPSYALHRDPKWTBEPKFLPERFSKKNQNDIPYITPPGSGPRNCTG 422
Db 383 GMPIPKGVVMMIPSYALHRDPKWTBEPKFLPERFSKKNQNDIPYITPPGSGPRNCTG 442
Qy 423 MRPALMMKALIRVLQNFSPKCKETQIPKLKSLGGLQPEKPVVLKVESRDGTVSGA 481
Db 443 MRPALMMKALIRVLQNFSPKCKETQIPKLKSLGGLQPEKPVVLKVESRDGTVSGA 501
```

RESULT 9

S50211
cytochrome P450 3A13 - mouse
N/Alternate names: oxidoreductase (EC 1.-.-.-)
C/Species: Mus musculus (house mouse)
C/Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: S50211; S18155
R/Yanagimoto, T.; Itoh, S.; Sawada, M.; Hashimoto, H.; Kametaki, T.
Biochim. Biophys. Acta 1201, 405-410, 1994
A/Title: Molecular cloning and functional expression of a mouse cytochrome P-450 (Cyp3a
A/Reference number: S50211; MUID:95101705; PMID:78034971
A/Accession: S50211
A/Molecule type: mRNA
A/Residues: 1-503 <YAN>
A/Cross-references: UNIPROT:Q64464; EMBL:X63023; NID:G50634; PIDN:CAA44754.1; PID:G5063
C/Genetic8:
A/Gene: CYP3A13
C/Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C/Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metal
F/302-464/Domain: cytochrome P450 homology <P45>
F/442/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 77.1%; Score 1961; DB 2; Length 503;
Best Local Similarity 75.7%; Pred. No. 8,6e-139;
Matches 361; Conservative 61; Mismatches 55; Indels 0; Gaps 0;

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Qy 3 YGTHSHGLFKKLGIPGTPPLPFLGNILSYHKGFCMPMECHKKYGKVMGFYDGOQVLA 62
Db 25 YGTHSHGLFKKLGIPGTPPLPFLGNILSYHKGFCMPMECHKKYGKVMGFYDGOQVLA 84
Qy 63 TDPDMIKTVLVKECYSFTRRRRPGVPYFPMKSAISIADEEMKRLRLSLPTFTSGKAKE 122
Db 85 TDPDMIKTVLVKECYSFTRRRRPGVPYFPMKSAISIADEEMKRLRLSLPTFTSGKAKE 144
Qy 123 MWPPIAAGDVLVNRNLRREAEATGKVTLLKDFGAYSMVITSTSGVNIIDSLNPPQDFV 182
Db 145 MWPPIAAGDVLVNRNLRREAEATGKVTLLKDFGAYSMVITSTSGVNIIDSLNPPQDFV 204
Qy 183 ENTKKLARFDLDPFLPSITVPFPLIPLEVLNLCVFPREVTNPLRKSVMKESRLDET 242
Db 205 ENTKKLARFDLDPFLPSITVPFPLIPLEVLNLCVFPREVTNPLRKSVMKESRLDET 264
Qy 243 QKRVDFLOLMIDSONSKETESHKALSDLEVAQSIIFIPAGYETTSVLSFIMYELATH 302
Db 265 QKRVDFLOLMIDSONSKETESHKALSDLEVAQSIIFIPAGYETTSVLSFIMYELATH 324
Qy 303 PDVQOKLOEIDAVLPNKAPPTVDTVLQMEYLDVNVNELLRLPPIAMLERVCKKQVEIN 362
Db 325 PDVQOKLOEIDAVLPNKAPPTVDTVLQMEYLDVNVNELLRLPPIAMLERVCKKQVEIN 384
Qy 363 GMPIPKGVVMMIPSYALHRDPKWTBEPKFLPERFSKKNQNDIPYITPPGSGPRNCTG 422
Db 385 GMPIPKGVVMMIPSYALHRDPKWTBEPKFLPERFSKKNQNDIPYITPPGSGPRNCTG 444
Qy 423 MRPALMMKALIRVLQNFSPKCKETQIPKLKSLGGLQPEKPVVLKVESRDGTVSGA 481
Db 445 MRPALMMKALIRVLQNFSPKCKETQIPKLKSLGGLQPEKPVVLKVESRDGTVSGA 501
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RESULT 10
Cytochrome P450 3A isoform, CYP3A43 protein - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-2001 #sequence_rev1sion 30-Jun-2001 #text_change 09-Jul-2004
C/Accession: J07627
R/Reslind, A.; Malnebo, S.; Johansson, I.; Oter, C.; Andersson, T.B.; Ingelman-Sunder
Biochem. Biophys. Res. Commun. 281, 1345-1355, 2001
A/Title: Cloning and tissue distribution of a novel human cytochrome P450 of the CYP3A
A/Reference number: J07627; MUID:21139777; PMID:11243885
A/Accession: J07627
A/Molecule type: mRNA
A/Residues: 1-503 <MSS>
A/Cross-references: UNIPROT:Q9H85; GB:AF337813
A/Comment: This CYP3A43 protein has broad and overlapping substrate specificities, and a
C/Genetics:
A/Genes: CYP3A43
A/Intons: 24/2; 55/3; 73/2; 106/3; 144/3; 174/2; 224/1; 266/3; 289/1; 342/3; 418/2; 472
C/Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C/Keywords: heme; iron; metalloprotein
P/442/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match          77.0%; Score 1957; DB 2; Length 503;
Best Local Similarity 76.2%; Pred. No. 1.7e-138;
Matches 364; Conservative 51; Mismatches 63; Indels 0; Gaps 0;

QY 3 YGTHSHGLPKKLGIPGPTPLPFLGNILSYHKFCMFDMCHKKYGKVGFGYDGOQVLA1 62
    |||||
DB 25 YGTHSHKLPKKGIPGPTPLPFLGTLFLYRLGMNFDRECKYGMWGLYEQQPMVL1 84
    |||||

QY 63 TDPMKITYLVKESYVFNNRRPFGVGFMSKASIADEEMKRLSLSPFTSGKLE 122
    |||||
DB 85 MDDPMKITYLVKESYVFNNRRPFGVGFMSKASIADEEMKRLSLSPFTSGKLE 144
    |||||

QY 123 MVDIIAQYGDVLRNLRREAEETGKPVTLKDFGAYSMVDITSTSGVINIDSLNPDPPV 182
    |||||
DB 145 MVDIISQCGDMLVRSIRQGEAKNSKSLNKKDFGAYMDVITGLFQGNIDSLNPDPPV 204
    |||||

QY 183 ENTKKILRPFLDPPFLSTVFPFLPILEVLNLCVPPRVNTPFKSVKMKESLEDT 242
    |||||
DB 205 KNNKKILKLDLPPFLSTVFPFLPILEVLNLCVPPRVNTPFKSVKMKESLEDT 264
    |||||

QY 243 QKRVDFLOLMIDSONSKETESHKALSDLEVAOSIIFPAGVETTSVLSFIMELATQ 302
    |||||
DB 265 QKRVDFLOLMIDSONSKETESHKALSDLEVAOSIIFPAGVETTSVLSFIMELATQ 324
    |||||

QY 303 PDVQOKLQGEIDAVLPKAPPTVDVLYOMEDLMVNETLRFPIMARLERVKQKVEIN 362
    |||||
DB 325 PDVQOKLQGEIDAVLPKAPPTVDVLYOMEDLMVNETLRFPIMARLERVKQKVEIN 384
    |||||

QY 363 GMFIPKGVVMISYALHRPKWTBPKFLPERFSKKNKONIDPIYTPFGSGPRNCIG 422
    |||||
DB 385 GVFIPKGLAVNVIYALHDPKWTBPKFLPERFSKKNKONIDPIYTPFGSGPRNCIG 444
    |||||

QY 423 MRPALMMKALIRVLONFSFKPKCKEQIPLKSLGSLQLOPEKPVVLAKVSRGATVSG 480
    |||||
DB 445 MRPALMMKALIRVLONFSFKPKCKEQIPLKSLGSLQLOPEKPVVLAKVSRGATVSG 502
    |||||

RESULT 11
A22631
Cytochrome P450 3A1, pregnenolone 16-alpha-carbonitrile-inducible - rat
N/Alternate names: testosterone 6beta-hydroxylase
C/Species: Rattus norvegicus (Norway rat)
C/Date: 29-Aug-1987 #sequence_rev1sion 29-Aug-1987 #text_change 09-Jul-2004
C/Accession: A22631; PX0035; S21697; S36137; S27107; S30378; I59218
R/Gonzalez, F.J.; Nebert, D.W.; Hardwick, J.P.; Kasper, C.B.
J. Biol. Chem. 260, 7435-7441, 1985
A/Title: Complete cDNA and protein sequence of a pregnenolone 16-alpha-carbonitrile-indu
A/Reference number: A22631; MUID:85207783; PMID:3838989
A/Accession: A22631
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A/Molecule type: mRNA
A/Residues: 1-504 <GON>
A/Cross-references: UNIPROT:P04800; GB:M10161; NID:9203777; P1DN:AAA41035.1; PID:9203778
R/Magata, K.; Gonzalez, F.J.; Yamazoe, Y.; Kato, R.
J. Biochem. 107, 718-725, 1990
A/Title: Purification and characterization of four catalytically active testosterone 6be
nally related forms.
A/Reference number: PX0032; MUID:90375438; PMID:2398038
A/Accession: PX0035
A/Molecule type: protein
A/Residues: 1-26 <NAG>
A/Experimental source: liver, Sprague-Dawley male rat
R/Lechner, M.C.
submitted to the EMBL Data Library, December 1991
A/Reference number: S21697
A/Accession: S21697
A/Molecule type: mRNA
A/Residues: 1-206, 'A', 208-212, 'I', 214-231, 'V', 233-504 <LEC>
A/Cross-references: EMBL:X64401; NID:956038; P1DN:CAA45743.1; PID:956039
R/Ribeiro, V.; Lechner, M.C.
Arch. Biochem. Biophys. 293, 147-152, 1992
A/Title: Cloning and characterization of a novel CYP3A1 allelic variant: Analysis of CYP
A/Reference number: S36137; MUID:92117688; PMID:1731631
A/Accession: S36137
A/Molecule type: mRNA
A/Residues: 205-206, 'A', 208-212, 'I', 214-231, 'V', 233-234 <RIB>
A/Cross-references: EMBL:X64401
R/Telhada, M.B.; Pereira, T.M.; Lechner, M.C.
Arch. Biochem. Biophys. 298, 715-725, 1992
A/Title: Effect of dexamethasone and phenobarbital on run-on transcription rate and CYP3
A/Reference number: S27107; MUID:93037516; PMID:1417000
A/Accession: S27107
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-24 <TEL>
A/Accession: S30378
A/Reference number: S30378; MUID:93213168; PMID:7681660
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-25 <COO>
R/Burger, H.
Proc. Natl. Acad. Sci. U.S.A. 89, 2145-2149, 1992
A/Title: Padoxical transcriptional activation of rat liver cytochrome P-450 3A1 by dex
to primary monolayer cultures of adult rat hepatocytes.
A/Reference number: I59218; MUID:92196074; PMID:1372436
A/Accession: I59218
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-24 <BUR>
A/Cross-references: GB:M86850; NID:9205919; P1DN:AAA41780.1; PID:9205920
C/Genetics:
A/Genes: CYP3A1; P450P
C/Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C/Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase,
P/303-465/Domain: cytochrome P450 homology <P45>
P/443/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match          76.6%; Score 1946.5; DB 2; Length 504;
Best Local Similarity 74.0%; Pred. No. 1e-137;
Matches 355; Conservative 62; Mismatches 62; Indels 1; Gaps 1;

QY 3 YGTHSHGLPKKLGIPGPTPLPFLGNILSYHKFCMFDMCHKKYGKVGFGYDGOQVLA1 62
    |||||
DB 25 YGTHSHKLPKKGIPGPTPLPFLGTLFLYRLGMNFDRECKYGMWGLYEQQPMVL1 84
    |||||

QY 63 TDPMKITYLVKESYVFNNRRPFGVGFMSKASIADEEMKRLSLSPFTSGKLE 122
    |||||
DB 85 MDDPMKITYLVKESYVFNNRRPFGVGFMSKASIADEEMKRLSLSPFTSGKLE 144
    |||||

QY 123 MVDIIAQYGDVLRNLRREAEETGKPVTLKDFGAYSMVDITSTSGVINIDSLNPDPPV 182
    |||||
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Db 145 MFPIEGYDILVYKLGQAEATGKVPYMKKVFAGYNSDVITSTFGNVDSLNPKDPFV 204
Qy 183 ENTYKLLRFPDLDFPFLSTIVPPLPILEVLNICEPREVTNFKSVKMKESRLDPT 242
Db 205 EKTQGLRFPFDPLFLSVLPPLTPYEMLNICMPKOSIEFFKVFVYMKETRLDSV 264
Qy 243 OKHRVDFLOLMIDSON-SKETESHKALSDLEVAOSIIFPAGETTSVLSFIMYELAT 301
Db 265 OKHRVDFLOLMIDSON-SKETESHKALSDLEVAOSIIFPAGETTSVLSFIMYELAT 324
Qy 302 HPDVQOKLOEIDAVLPNKAPPTVDYVLOMEYLDVMVNETLRLPIMARLERVCKDVEI 361
Db 325 HPDVQOKLOEIDAVLPNKAPPTVDYVLOMEYLDVMVNETLRLPIMARLERVCKDVEI 384
Qy 362 NGMFIPGVVVMIPSYALHRDPKYTWEPKFLPERFSKKNKNDIPYIYTPFGSGPRNCI 421
Db 385 NGVFMFGSVVMIPSYALHRDPQHWPEPEPRPERFSKKNKNDIPYIYTPFGSGPRNCI 444
Qy 422 GMPFALMMMLALIRVONFSFKCKETOTPLKLSGLLOPEKPVVLKXESRGTYSGA 481
Db 445 GMPFALMMMLALIRVONFSFKCKETOTPLKLSGLLOPEKPVVLKXESRGTYSGA 504

RESULT 12

A29487
cytochrome P450 3A6 (version 1) - rabbit
N/Alternate names: cytochrome P450 3c
N/Contains: oxidoreductase (EC 1.-.-.-)
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C/Accession: A29487
R/Daler, C.; Clair, P.; Dautat, M.; Fort, P.; Blanchard, J.M.; Maurel, P.
DNA 7, 39-46, 1988
A/Title: Complete sequence of cytochrome P450 3c cDNA and presence of two mRNA species
A/Reference number: A29487; MUID:88166352; PMID:3349903
A/Accession: A29487
A/Molecule type: mRNA
A/Residues: 1501 <DAL>
A/Cross-references: UNIPROT:P11707; GB:M19139; NID:G165573; PIDN:AAA31430.1; PID:G165574
C/Gene: CYP3A6
C/Suprafamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C/Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
P/301-462/Domain: cytochrome P450 homology <P45>
P/440/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 76.2%; Score 1937; DB 2; Length 501;
Best Local Similarity 74.8%; Pred. No. 5,3e-137;
Matches 359; Conservative 63; Mismatches 56; Indels 2; Gaps 2;
Qy 3 YGTHSHGLFKKGIIPGPTPLPFLGNILSYHKGFCM-FDMECHKKYGKVGFGYDGOQPLAT 61
Db 23 YGTHSHGLFKKGIIPGPTPLPFLGNILSYHKGFCM-FDMECHKKYGKVGFGYDGOQPLAT 82
Qy 62 IDPDMIKTVLVKCEYVFNNRRPFGVGMKSAISIAEDBEWKRLSLSPPTSGTKL 121
Db 83 IDPDMIKTVLVKCEYVFNNRRPFGVGMKSAISIAEDBEWKRLSLSPPTSGTKL 142
Qy 122 EMPPIAQGDVAVRNLRBAETGKPYTLKDVFGAYSMDVITSTFGVNIDSINNPDPFV 181
Db 143 EMPPIAQGDVAVRNLRBAETGKPYTLKDVFGAYSMDVITSTFGVNIDSINNPDPFV 202
Qy 182 VENTTKLRFDFLDFPFLSTIVPPLPILEVLNICEPREVTNFKSVKMKESRLD 241
Db 203 VENTTKLRFDFLDFPFLSTIVPPLPILEVLNICEPREVTNFKSVKMKESRLD 262
Qy 242 TOGHRVDFLOLMIDSON-SKETESHKALSDLEVAOSIIFPAGETTSVLSFIMYELAT 301
Db 263 TOGHRVDFLOLMIDSON-SKETESHKALSDLEVAOSIIFPAGETTSVLSFIMYELAT 322
Qy 302 HPDVQOKLOEIDAVLPNKAPPTVDYVLOMEYLDVMVNETLRLPIMARLERVCKDVEI 361

Db 323 HPDVQOKLOEIDAVLPNKAPPTVDYVLOMEYLDVMVNETLRLPIMARLERVCKDVEI 382
Qy 362 NGMFIPGVVVMIPSYALHRDPKYTWEPKFLPERFSKKNKNDIPYIYTPFGSGPRNCI 421
Db 383 NGVFMFGSVVMIPSYALHRDPQHWPEPEPRPERFSKKNKNDIPYIYTPFGSGPRNCI 441
Qy 422 GMPFALMMMLALIRVONFSFKCKETOTPLKLSGLLOPEKPVVLKXESRGTYSGA 481
Db 445 GMPFALMMMLALIRVONFSFKCKETOTPLKLSGLLOPEKPVVLKXESRGTYSGA 501

RESULT 13

A60564
cytochrome P450 3A11 - mouse
N/Alternate names: cytochrome P450 3A-UT; cytochrome P450 11A1
N/Contains: oxidoreductase (EC 1.-.-.-)
C/Species: Mus musculus (house mouse)
C/Date: 17-Apr-1993 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C/Accession: S22334; A60564
R/Yanagimoto, T.; Itoh, S.; Muller-Eberhard, D.; Kametani, T.
Biochim. Biophys. Acta 1130, 329-332, 1992
A/Title: Mouse liver cytochrome P-450 (P-45011A1): its cDNA cloning and inducibility
A/Reference number: S22334; MUID:9223116; PMID:1339292
A/Accession: S22334
A/Molecule type: mRNA
A/Residues: 1504 <YAN>
A/Cross-references: UNIPROT:Q64459; EMBL:X60452; NID:950534; PIDN:CAA42981.1; PID:95053
R/Bornheim, L.M.; Correia, M.A.
Mol. Pharmacol. 38, 319-326, 1990
A/Title: Selective inactivation of mouse liver cytochrome P-45011A by cannabidiol.
A/Reference number: A60564; MUID:90384441; PMID:2402224
A/Accession: A60564
A/Molecule type: protein
A/Residues: 1-17, 'X', 19-20, 'X', 22-24 <BOR>
A/Comment: This member of the cytochrome P45011A family was designated UT because it c
laction of testosterone.
C/Gene: CYP3A11
C/Suprafamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C/Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metal
P/303-465/Domain: cytochrome P450 homology <P45>
P/443/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 76.1%; Score 1935.5; DB 2; Length 504;
Best Local Similarity 73.1%; Pred. No. 6,9e-137;
Matches 351; Conservative 64; Mismatches 64; Indels 1; Gaps 1;
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Db 25 YGTHSHGLFKKGIIPGPTPLPFLGNILSYHKGFCM-FDMECHKKYGKVGFGYDGOQPLAT 84
Qy 63 IDPDMIKTVLVKCEYVFNNRRPFGVGMKSAISIAEDBEWKRLSLSPPTSGTKL 122
Db 85 IDPDMIKTVLVKCEYVFNNRRPFGVGMKSAISIAEDBEWKRLSLSPPTSGTKL 144
Qy 123 EMPPIAQGDVAVRNLRBAETGKPYTLKDVFGAYSMDVITSTFGVNIDSINNPDPFV 182
Db 145 EMPPIAQGDVAVRNLRBAETGKPYTLKDVFGAYSMDVITSTFGVNIDSINNPDPFV 204
Qy 183 ENTYKLLRFPDLDFPFLSTIVPPLPILEVLNICEPREVTNFKSVKMKESRLD 242
Db 205 ENTYKLLRFPDLDFPFLSTIVPPLPILEVLNICEPREVTNFKSVKMKESRLD 264
Qy 243 OKHRVDFLOLMIDSON-SKETESHKALSDLEVAOSIIFPAGETTSVLSFIMYELAT 301
Db 265 OKHRVDFLOLMIDSON-SKETESHKALSDLEVAOSIIFPAGETTSVLSFIMYELAT 324
Qy 302 HPDVQOKLOEIDAVLPNKAPPTVDYVLOMEYLDVMVNETLRLPIMARLERVCKDVEI 361
Db 325 HPDVQOKLOEIDAVLPNKAPPTVDYVLOMEYLDVMVNETLRLPIMARLERVCKDVEI 384
Qy 362 NGMFIPGVVVMIPSYALHRDPKYTWEPKFLPERFSKKNKNDIPYIYTPFGSGPRNCI 421

DB 385 NGVYIEKSGTVMIPSYALHHDDPQMSRBEERQPERFSEKNGSIDPYYVLLPFGNPRNCL 444

QY 422 GKRFAIMNNKALIRVLQNFSPKPKCKETQIPLKISLGLLOPKRPVILKVESRDGTVSGA 481

DB 445 GKRFAIMNNKALIRVLQNFSPKPKCKETQIPLKISLGLLOPKRPVILKVESRDGTVSGA 504

RESULT 14

A25222

Cytochrome P450 3A2 - rat

N:Alternate names: cytochrome P450CN2, pregnenolone 16- α -carbonitrile-inducible; tes

N:Contains: oxidoreductase (EC 1.-.-.-)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 05-Oct-1988 #sequence revision 05-Oct-1988 #text change 09-Jul-2004

C:Accession: A25222; S27108; S46938; PX0034; S30379

R:Gonzalez, F.J.; Song, B.-J.; Hardwick, J.P.

Mol. Cell. Biol. 6, 2969-2976, 1986

A:Title: Pregnenolone 16- α -carbonitrile-inducible P-450 gene family: gene conversion

A:Reference number: A25222; PMID:87064606; PMID:3785219

A:Accession: A25222

A:Molecule type: mRNA

A:Residues: 1-504 <CON>

A:Cross-references: UNIPROT:P05183; GB:M13646; NID:9203827; PIDN:AAA41051.1; PID:g203828

A:Note: the authors translated the codon GAC for residue 445 as Gly

R:Telhada, M.B.; Pereira, T.M.; Lechner, M.C.

Arch. Biochem. Biophys. 298, 715-725, 1992

A:Title: Effect of dexamethasone and phenobarbital on run-on transcription rate and CYP3

A:Reference number: S27107; PMID:93037516; PMID:1417000

A:Accession: S27108

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-36 <TEL>

A:Cross-references: EMBL:X62087

R:Miya, M.; Nagata, K.; Shimada, M.; Yamazoe, Y.; Kato, R.

A:Description: Structure of a gene and cDNA of a major constitutive form of testosterone

A:Reference number: S46938

A:Accession: S46938

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-428, 'D', 430-444, 'G', 446-504 <MY>

A:Cross-references: EMBL:X79320; NID:9515381; PIDN:CA55888.1; PID:g515382

R:Nagata, K.; Gonzalez, F.J.; Yamazoe, Y.; Kato, R.

J. Biochem. 107, 718-725, 1990

A:Title: Purification and characterization of four catalytically active testosterone 6 β

A:Reference number: PX0032; PMID:90375438; PMID:2398038

A:Accession: PX0032

A:Molecule type: protein

A:Residues: 1-21, 'X', 23-26, 'X', 28-29, 'X', 31-33 <NAG>

A:Experimental source: liver, Sprague-Dawley male rat

A:Accession: PX0034

A:Molecule type: protein

A:Residues: 1-27, 'X', 29, 'X', 31-33 <N2>

R:Cooper, K.O.; Reik, L.M.; Jayosi, Z.; Bandiera, S.; Kelley, M.; Ryan, D.E.; Daniel, R

Arch. Biochem. Biophys. 301, 345-354, 1993

A:Title: Regulation of two members of the steroid-inducible cytochrome P450 subfamily (3

A:Reference number: S30378; PMID:93213168; PMID:7681660

A:Accession: S30379

A:Molecule type: protein

A:Residues: 1-25 <COO>

C:Genetic:

A:Gene: CYP3A2

A:introns: 24/2

A:Note: this list of introns is incomplete

C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology

C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;

F303-465; Domain: cytochrome P450 homology <45>

F443/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 74.9%; Score 1904.5; DB 2; Length 504;

Best Local Similarity 72.2%; Pred. No. 1.4e-134;

Matches 346; Conservative 68; Mismatches 64; Indels 1; Gaps 1;

[illegible]

```

RESULT 15
JX0334
cytochrome P450 3A RL33 - rat
N:Contains: oxidoreductase (EC 1.-.-.-)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C:Accession: JX0334; S39797
R:Komori, M.; Oda, Y.
U: Biochem. 116, 114-120, 1994
A:Title: A major glucocorticoid-inducible P450 in rat liver is not P450 3A1.
A:Reference number: JX0334; PMID:95096005; PMID:7528203
A:Accession: JX0334
A:Molecule type: mRNA
A:Residues: 1-502 <K0M>
A:Cross-references: UNIPROT:Q06884; GB:D29967; NID:G479038; PIDN:BA06233.1; PID:G479039
A:Experimental source: Liver
R:Kiritla, S.; Matsubara, T.
Arch. Biochem. Biophys. 307, 253-258, 1993
A:Title: cDNA cloning and characterization of a novel member of steroid-induced cytochrome
A:Reference number: S39797; PMID:94059605; PMID:8274011
A:Accession: S39797
A:Molecule type: mRNA
A:Residues: 1-106, 'D', 108-502 <KIR>
A:Cross-references: EMBL:DJ3912; NID:G220835; PIDN:BA03008.1; PID:G220836; GB:X96721; N
C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C:Keywords: chromoprotein; heme; iron; metalloprotein; monooxygenase; oxidoreductase; tr
F:J01.465/Domain: cytochrome P450 homology <P45>
F:J41/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match          74.8%; Score 1902.5; DB 2; Length 502;
Best Local Similarity 72.5%; Pred. No. 2e-134;
Matches 348; Conservative 64; Mismatches 65; Indels 3; Gaps 2;

QY      3 YGTHSHGLFKKGIIGPTPLPFLGNILSYHKGFCEMFMECHKKYKGVWGFYDQGPVIAI 62
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Db      25 FGRTGGLPKKGGIPEPKPLPFPGVTLYNWGLMKPFVECHKYCKGIKGLFDGGMPLFAI 84

QY      63 TDPDMIKTVLVNCEYVFTFNRRPFGPYGVGFKSAISIADEDEWKRRLSLSPFTTSGLKE 122
      ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

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Db 85 TDTEMKXVLYBECPSVFTNRRYFGVPGVGMGKAISVSKDEEMKRYRALLSPFTISGRUKE 144

Qy 123 MVEPIIAQYGDVLYNRLRREATGKPYTLKDYFGAYSMDVITSTSPGVNIDSLNPDPPV 182

Db 145 MPVIEQYGDILVKKYLRQ-EKGKEVPYKAEVFGAYSMDVITSTSPGVNIDSLNPDPPV 202

Qy 183 ENTKKLAFDPLDPPFLSITVPPFLIFILEVLNLCVPPREVTNFIKRSVKRMKKSRLDPT 242

Db 203 EKAKKLLRIFDPLFLSVLPPFLTPVYEMLNICMPPKDSIEFPKFFVYRMKKTRLDSV 262

Qy 243 QKHRVDFLOLMIDSON-SKETESHKALSDLEIVAQSIIFIPAGYETTSSVLSPIWYELAT 301

Db 263 QKHRVDFLOLMNHNNDKSHSTALSDMEITAGSIIFIPAGYERTSTISFVLHSLAT 322

Qy 302 HPDVQOKLOEBIDAVLPKAPPTTYDTVLOMEYLDNVTNETLRPIANRLERVCCKOYEI 361

Db 323 HPDQOKLOEBIDRALPKAPPTTYDTVMEWEMEYLDVNLNETLRPIGNRLERVCCKOYEI 382

Qy 362 NGMFLPKGVVMIPSYALHRDPKWTBEPKFLPBRFSKKNONTDPIYLYTPGSGPRNCI 421

Db 383 NGVEMPKGSVVMIPSYALHRDPOHWPBEPBEPKPERFSKKNKGSIDPIVYLLPFGNGPRNCI 442

Qy 422 GMRPALMMKALIRVLQNFSPKCKEIQIPKLISGLQPEKPVVLKVESRDGTVSGA 481

Db 443 GMRPALMMKALIRVLQNFSPKCKEIQIPKLISGLQPTKPIILKVVPRDEIITGS 502

Search completed: July 8, 2005, 14:14:16
Job time : 43 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2005, 14:14:33 ; Search time 166 Seconds

(without alignments)
1128.736 Million cell updates/sec

Title: US-10-690-991-2

Perfect score: 2542
Sequence: 1 MACTGSHGLFKKLGIGPPT.....PVLKVESRDGTSGAHHH 485

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1726216 seqs, 38630316 residues

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubppaa/PC7_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2542	100.0	485	US-10-690-991-2	Sequence 2, Appl1
2	2542	100.0	485	US-10-833-296-2	Sequence 2, Appl1
3	2501	98.4	503	US-10-313-963A-56	Sequence 56, Appl1
4	2494	98.1	503	US-10-146-575-2	Sequence 2, Appl1
5	2449.5	96.4	504	US-10-804-772-24	Sequence 24, Appl1
6	2372	93.3	503	US-10-732-923-1079	Sequence 1079, Ap
7	2233	87.8	503	US-09-957-997-3	Sequence 3, Appl1
8	2011.5	79.1	499	US-10-626-686-66	Sequence 66, Appl1
9	1958	77.0	502	US-10-274-694-7	Sequence 7, Appl1
10	1958	77.0	502	US-10-332-448-7	Sequence 7, Appl1
11	1957	77.0	503	US-10-007-614-2	Sequence 2, Appl1

12	1956	76.9	503	US-10-112-944-432	Sequence 432, App
13	1946.5	76.6	504	US-10-007-814-4	Sequence 4, Appl1
14	1882	74.0	508	US-10-274-694-16	Sequence 16, Appl1
15	1882	74.0	508	US-10-332-448-16	Sequence 16, Appl1
16	1620	63.7	420	US-10-007-814-6	Sequence 6, Appl1
17	905	33.6	217	US-10-106-698-6001	Sequence 6001, Ap
18	840.5	33.1	534	US-10-087-192-2004	Sequence 2004, Ap
19	840.5	33.1	534	US-10-741-601-291	Sequence 291, App
20	840.5	33.1	534	US-10-741-601-292	Sequence 292, App
21	832.5	32.7	515	US-10-732-923-1068	Sequence 1068, Ap
22	824.5	32.4	533	US-10-087-192-2001	Sequence 2001, Ap
23	802	31.5	250	US-10-007-814-8	Sequence 8, Appl1
24	678.5	26.7	518	US-10-732-923-1069	Sequence 1069, Ap
25	668.5	26.3	466	US-09-945-301-4	Sequence 4, Appl1
26	668.5	26.3	466	US-10-067-668-10	Sequence 10, Appl1
27	668.5	26.3	466	US-10-175-696-10	Sequence 10, Appl1
28	668.5	26.3	466	US-10-776-871-10	Sequence 10, Appl1
29	668.5	26.3	496	US-10-782-695-19	Sequence 19, Appl1
30	659.5	25.9	445	US-10-032-189-73	Sequence 73, Appl1
31	659.5	25.9	445	US-10-072-012-848	Sequence 848, App
32	658.5	25.9	440	US-10-074-978A-209	Sequence 209, App
33	658.5	25.9	460	US-10-741-601-293	Sequence 293, App
34	631	24.8	470	US-10-067-668-12	Sequence 12, Appl1
35	631	24.8	470	US-10-175-696-12	Sequence 12, Appl1
36	631	24.8	470	US-10-776-871-12	Sequence 12, Appl1
37	623	24.5	520	US-10-369-493-5530	Sequence 5530, Ap
38	620.5	24.4	519	US-10-369-493-5529	Sequence 5529, Ap
39	610.5	24.0	423	US-10-231-913-274	Sequence 274, App
40	594	23.4	520	US-10-369-493-5531	Sequence 5531, Ap
41	591.5	23.3	518	US-10-369-493-5532	Sequence 5532, Ap
42	590.5	23.2	510	US-10-021-425-36	Sequence 36, Appl1
43	590.5	23.2	510	US-10-369-493-5677	Sequence 5677, Ap
44	590.5	23.2	510	US-10-900-856-39	Sequence 39, Appl1
45	588.5	23.2	522	US-10-369-493-5678	Sequence 5678, Ap

ALIGNMENTS

RESULT 1
US-10-690-991-2
Sequence 2, Appl1
Publication No. US2004023319A1
GENERAL INFORMATION:
APPLICANT: Tickle, Ian J
APPLICANT: Vonrhein, Clemens
APPLICANT: Williams, Pamela A
APPLICANT: Jhoti, Harren
APPLICANT: Kirtton, Stewart Brian
TITLE OF INVENTION: Crystal structure of cytochrome P450
FILE REFERENCE: 620-282
CURRENT APPLICATION NUMBER: US/10/690,991
CURRENT FILING DATE: 2004-04-13
PRIOR APPLICATION NUMBER: US 60/421,063
PRIOR FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: PCT/GB02/02668
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: US 10/221,036
PRIOR FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: US 60/479,448
PRIOR FILING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 485
TYPE: PRT
ORGANISM: Artificial sequence
FEATURES:
OTHER INFORMATION: Human J34 P450 protein truncated in its N-terminal region to
OTHER INFORMATION: delete the hydrophobic trans-membrane domain, and the region
US-10-690-991-2

Query Match 100.0%; Score 2542; DB 16; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.6e-218;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MAYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGCMFDMCHKKYKGYWGFYDGOQPYL 60
DB 61 ATDPDMITKTVLKECYSVFTNRPRPGVGFPMKSAISIAEDBEWKRLSLSPFTSGKL 120
61 ATDPDMITKTVLKECYSVFTNRPRPGVGFPMKSAISIAEDBEWKRLSLSPFTSGKL 120
DB 61 ATDPDMITKTVLKECYSVFTNRPRPGVGFPMKSAISIAEDBEWKRLSLSPFTSGKL 120
QY 121 KEMVPIIAQYGDVLYRNLRREAETGKPTLKDVFGAYSMDVITSTSGVNIIDSLNPPDP 180
121 KEMVPIIAQYGDVLYRNLRREAETGKPTLKDVFGAYSMDVITSTSGVNIIDSLNPPDP 180
DB 121 KEMVPIIAQYGDVLYRNLRREAETGKPTLKDVFGAYSMDVITSTSGVNIIDSLNPPDP 180
QY 181 FVENTKLLRPDLPFLPSITVFPPLIPLEVLNICVFPREVTNFLRKSVMKESRL 240
181 FVENTKLLRPDLPFLPSITVFPPLIPLEVLNICVFPREVTNFLRKSVMKESRL 240
DB 181 FVENTKLLRPDLPFLPSITVFPPLIPLEVLNICVFPREVTNFLRKSVMKESRL 240
QY 241 DTQKRVDPFLQMLIDSONSKETESHKALSDLELVAOSIIFIPAGYETTSSVLSFTMYELA 300
241 DTQKRVDPFLQMLIDSONSKETESHKALSDLELVAOSIIFIPAGYETTSSVLSFTMYELA 300
DB 241 DTQKRVDPFLQMLIDSONSKETESHKALSDLELVAOSIIFIPAGYETTSSVLSFTMYELA 300
QY 301 THPDVQOKLQOEIDAVLPNKAPPTVDVLOMEYLDVMVNETLRLPIARLERVCKDVE 360
301 THPDVQOKLQOEIDAVLPNKAPPTVDVLOMEYLDVMVNETLRLPIARLERVCKDVE 360
DB 301 THPDVQOKLQOEIDAVLPNKAPPTVDVLOMEYLDVMVNETLRLPIARLERVCKDVE 360
QY 361 INGMFIPKGVVVMIPSYALHRDPKYTEBEKFLPERFSKKNKNDIDPIYTPFGSGPRNC 420
361 INGMFIPKGVVVMIPSYALHRDPKYTEBEKFLPERFSKKNKNDIDPIYTPFGSGPRNC 420
DB 361 INGMFIPKGVVVMIPSYALHRDPKYTEBEKFLPERFSKKNKNDIDPIYTPFGSGPRNC 420
QY 421 IGMRFALNMKALIRVLONFSFKCKETOIPLKSLGGLQPEKRVYLKVESRDGTVSG 480
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DB 481 AHHHH 485

RESULT 2
US-10-833-296-2
; Sequence 2, Application US/10833296
; Publication No. US20050032119A1
; GENERAL INFORMATION:
; APPLICANT: Tickle, Ian J
; APPLICANT: Vonthlein, Clemens
; APPLICANT: Vankovic, Dijana M
; APPLICANT: Kliron, Stewart
; APPLICANT: Williams, Pamela A
; APPLICANT: Jhoti, Harren
; TITLE OF INVENTION: Crystall Structure of Cytochrome P450
; FILE REFERENCE: 620-305
; CURRENT APPLICATION NUMBER: US/10/833,296
; CURRENT FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: GB 0108214.8
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: GB 0108212.2
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/479,448
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/421,063
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/306,873
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/306,874
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 10/690,991
; PRIOR FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 10/221,036
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: PCT/GB02/02668

; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 485
; TYPE: PR
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human 3A4 P450 protein truncated in its N-terminal region
; OTHER INFORMATION: to delete the hydrophobic trans-membrane domain, and the
; OTHER INFORMATION: region replaced by a short N-terminal sequence.
US-10-833-296-2

Query Match 100.0%; Score 2542; DB 17; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.6e-218;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGCMFDMCHKKYKGYWGFYDGOQPYL 60
1 MAYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGCMFDMCHKKYKGYWGFYDGOQPYL 60
DB 61 ATDPDMITKTVLKECYSVFTNRPRPGVGFPMKSAISIAEDBEWKRLSLSPFTSGKL 120
61 ATDPDMITKTVLKECYSVFTNRPRPGVGFPMKSAISIAEDBEWKRLSLSPFTSGKL 120
DB 61 ATDPDMITKTVLKECYSVFTNRPRPGVGFPMKSAISIAEDBEWKRLSLSPFTSGKL 120
QY 121 KEMVPIIAQYGDVLYRNLRREAETGKPTLKDVFGAYSMDVITSTSGVNIIDSLNPPDP 180
121 KEMVPIIAQYGDVLYRNLRREAETGKPTLKDVFGAYSMDVITSTSGVNIIDSLNPPDP 180
DB 121 KEMVPIIAQYGDVLYRNLRREAETGKPTLKDVFGAYSMDVITSTSGVNIIDSLNPPDP 180
QY 181 FVENTKLLRPDLPFLPSITVFPPLIPLEVLNICVFPREVTNFLRKSVMKESRL 240
181 FVENTKLLRPDLPFLPSITVFPPLIPLEVLNICVFPREVTNFLRKSVMKESRL 240
DB 181 FVENTKLLRPDLPFLPSITVFPPLIPLEVLNICVFPREVTNFLRKSVMKESRL 240
QY 241 DTQKRVDPFLQMLIDSONSKETESHKALSDLELVAOSIIFIPAGYETTSSVLSFTMYELA 300
241 DTQKRVDPFLQMLIDSONSKETESHKALSDLELVAOSIIFIPAGYETTSSVLSFTMYELA 300
DB 241 DTQKRVDPFLQMLIDSONSKETESHKALSDLELVAOSIIFIPAGYETTSSVLSFTMYELA 300
QY 301 THPDVQOKLQOEIDAVLPNKAPPTVDVLOMEYLDVMVNETLRLPIARLERVCKDVE 360
301 THPDVQOKLQOEIDAVLPNKAPPTVDVLOMEYLDVMVNETLRLPIARLERVCKDVE 360
DB 301 THPDVQOKLQOEIDAVLPNKAPPTVDVLOMEYLDVMVNETLRLPIARLERVCKDVE 360
QY 361 INGMFIPKGVVVMIPSYALHRDPKYTEBEKFLPERFSKKNKNDIDPIYTPFGSGPRNC 420
361 INGMFIPKGVVVMIPSYALHRDPKYTEBEKFLPERFSKKNKNDIDPIYTPFGSGPRNC 420
DB 361 INGMFIPKGVVVMIPSYALHRDPKYTEBEKFLPERFSKKNKNDIDPIYTPFGSGPRNC 420
QY 421 IGMRFALNMKALIRVLONFSFKCKETOIPLKSLGGLQPEKRVYLKVESRDGTVSG 480
421 IGMRFALNMKALIRVLONFSFKCKETOIPLKSLGGLQPEKRVYLKVESRDGTVSG 480
DB 421 IGMRFALNMKALIRVLONFSFKCKETOIPLKSLGGLQPEKRVYLKVESRDGTVSG 480
QY 481 AHHHH 485
481 AHHHH 485
DB 481 AHHHH 485

RESULT 3
US-10-313-963A-56
; Sequence 56, Application US/10313963A
; Publication No. US2004002078A1
; GENERAL INFORMATION:
; APPLICANT: Boulell, Jonathan
; APPLICANT: Godber, Benjamin
; APPLICANT: Hart, Darren
; APPLICANT: Blackburn, Jonathan
; TITLE OF INVENTION: Arrays
; FILE REFERENCE: KIL-001
; CURRENT APPLICATION NUMBER: US/10/313,963A
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/335,806
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/410,815
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1

SEQ ID NO 56
LENGTH: 503
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-313-963A-56

Query Match 98.4%; Score 2501; DB 15; Length 503;
Best Local Similarity 100.0%; Pred. No. 1,7e-214;
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFMECHKKYGVWGFYDGOQPLAI 62
DB 25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFMECHKKYGVWGFYDGOQPLAI 84
QY 63 TDPDMIKTVLVKCEYSVFTNRPRPGVGFPMKSAISIADEBWKRLSLSPFTSGDLKE 122
DB 85 TDPDMIKTVLVKCEYSVFTNRPRPGVGFPMKSAISIADEBWKRLSLSPFTSGDLKE 144
QY 123 MNPILIAQGVDLVNRNLRREAEKGPVTLKOVFGAYSMDVITSTSGVNIIDSLNPPDPFV 182
DB 145 MNPILIAQGVDLVNRNLRREAEKGPVTLKOVFGAYSMDVITSTSGVNIIDSLNPPDPFV 204
QY 183 ENTKKLRFDFLDPFLSTIVFPFLIPLEVLNICVFPREVTNFKRSVKRMKESRLDET 242
DB 205 ENTKKLRFDFLDPFLSTIVFPFLIPLEVLNICVFPREVTNFKRSVKRMKESRLDET 264
QY 243 QKRVDFLQMLMIDSONSKETESHKALSDLEVAOSIIFIFAGYETTSVLSFIWEELATH 302
DB 265 QKRVDFLQMLMIDSONSKETESHKALSDLEVAOSIIFIFAGYETTSVLSFIWEELATH 324
QY 303 PDVQOKLQEBIDALPNKAPPTVDTVLQMEYLDVNVNETHLRFPIAMRLERVCCKDVEIN 362
DB 325 PDVQOKLQEBIDALPNKAPPTVDTVLQMEYLDVNVNETHLRFPIAMRLERVCCKDVEIN 384
QY 363 GMFIPKGVVWMIPSYALHRDPKWTBPEKFLPERFSKKNKONIDPIYITPFGSGPRNCIG 422
DB 385 GMFIPKGVVWMIPSYALHRDPKWTBPEKFLPERFSKKNKONIDPIYITPFGSGPRNCIG 444
QY 423 MRPALMMKALIRVLQNFSPCKEQTQIPKLKSLGGLQPEKRVVLKVESRDGTSGA 481
DB 445 MRPALMMKALIRVLQNFSPCKEQTQIPKLKSLGGLQPEKRVVLKVESRDGTSGA 503

RESULT 4
US-10-146-575-2
Sequence 2, Application US/10146575
Publication No. US20030059800A1
GENERAL INFORMATION:
APPLICANT: Lichter, Jay
APPLICANT: Guido, Marco
TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
FILE REFERENCE: SEQ-12P
CURRENT APPLICATION NUMBER: US/10/146,575
CURRENT FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: US/09/144,367
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 503
TYPE: PRT
ORGANISM: H. sapiens
US-10-146-575-2

Query Match 98.1%; Score 2494; DB 14; Length 503;
Best Local Similarity 99.8%; Pred. No. 7,4e-214;
Matches 479; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFMECHKKYGVWGFYDGOQPLAI 62
DB 25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFMECHKKYGVWGFYDGOQPLAI 84
QY 63 TDPDMIKTVLVKCEYSVFTNRPRPGVGFPMKSAISIADEBWKRLSLSPFTSGDLKE 122

DB 85 TDPDMIKTVLVKCEYSVFTNRPRPGVGFPMKSAISIADEBWKRLSLSPFTSGDLKE 144
QY 123 MNPILIAQGVDLVNRNLRREAEKGPVTLKOVFGAYSMDVITSTSGVNIIDSLNPPDPFV 182
DB 145 MNPILIAQGVDLVNRNLRREAEKGPVTLKOVFGAYSMDVITSTSGVNIIDSLNPPDPFV 204
QY 183 ENTKKLRFDFLDPFLSTIVFPFLIPLEVLNICVFPREVTNFKRSVKRMKESRLDET 242
DB 205 ENTKKLRFDFLDPFLSTIVFPFLIPLEVLNICVFPREVTNFKRSVKRMKESRLDET 264
QY 243 QKRVDFLQMLMIDSONSKETESHKALSDLEVAOSIIFIFAGYETTSVLSFIWEELATH 302
DB 265 QKRVDFLQMLMIDSONSKETESHKALSDLEVAOSIIFIFAGYETTSVLSFIWEELATH 324
QY 303 PDVQOKLQEBIDALPNKAPPTVDTVLQMEYLDVNVNETHLRFPIAMRLERVCCKDVEIN 362
DB 325 PDVQOKLQEBIDALPNKAPPTVDTVLQMEYLDVNVNETHLRFPIAMRLERVCCKDVEIN 384
QY 363 GMFIPKGVVWMIPSYALHRDPKWTBPEKFLPERFSKKNKONIDPIYITPFGSGPRNCIG 422
DB 385 GMFIPKGVVWMIPSYALHRDPKWTBPEKFLPERFSKKNKONIDPIYITPFGSGPRNCIG 444
QY 423 MRPALMMKALIRVLQNFSPCKEQTQIPKLKSLGGLQPEKRVVLKVESRDGTSGA 481
DB 445 MRPALMMKALIRVLQNFSPCKEQTQIPKLKSLGGLQPEKRVVLKVESRDGTSGA 503

RESULT 5
US-10-804-772-24
Sequence 24, Application US/10804772
Publication No. US20040244077A1
GENERAL INFORMATION:
APPLICANT: Azpiroz, Ricardo
APPLICANT: Choe, Sungwa
TITLE OF INVENTION: DMPA POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: 11696-070001
CURRENT APPLICATION NUMBER: US/10/804,772
CURRENT FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: US/09/502,426
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/119,657
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: US 60/119,658
PRIOR FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 504
TYPE: PRT
ORGANISM: Homo sapiens
US-10-804-772-24

Query Match 96.4%; Score 2449.5; DB 16; Length 504;
Best Local Similarity 97.9%; Pred. No. 7e-210;
Matches 470; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFMECHKKYGVWGFYDGOQPLAI 62
DB 25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFMECHKKYGVWGFYDGOQPLAI 84
QY 63 TDPDMIKTVLVKCEYSVFTNRPRPGVGFPMKSAISIADEBWKRLSLSPFTSGDLKE 122
DB 85 TDPDMIKTVLVKCEYSVFTNRPRPGVGFPMKSAISIADEBWKRLSLSPFTSGDLKE 144
QY 123 MNPILIAQGVDLVNRNLRREAEKGPVTLKOVFGAYSMDVITSTSGVNIIDSLNPPDPFV 182
DB 145 MNPILIAQGVDLVNRNLRREAEKGPVTLKOVFGAYSMDVITSTSGVNIIDSLNPPDPFV 204
QY 183 ENTKKLRFDFLDPFLSTIVFPFLIPLEVLNICVFPREVTNFKRSVKRMKESRLDET 242
DB 205 ENTKKLRFDFLDPFLSTIVFPFLIPLEVLNICVFPREVTNFKRSVKRMKESRLDET 264

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QY 243 QKRVDFLOLMIDS -QNSKTESHKAISDELVAOSIIIFAGYETTSSVLSFIMELAT 301
DB 265 QKRVDFLOLMIDS HSHKTESHKAISDELVAOSIIIFAGYETTSSVLSFIMELAT 324
QY 302 HPVQOKLOEIDAVLPNKAPPTVDVLOMEYLDVMVNETLRPLFPIAMLERVCKKDOVEI 361
DB 325 HPVQOKLOEIDAVLPNKAPPTVDVLOMEYLDVMVNETLRPLFPIAMLERVCKKDOVEI 384
QY 362 NGMFIPKGVVMI PSYALHBDPKWTEPEKFLPERFSKKNKONIDPIYITPFGSGPRNCI 421
DB 385 NGMFIPKGVVMI PSYALHBDPKWTEPEKFLPERFSKKNKONIDPIYITPFGSGPRNCI 444
QY 422 GMEFALNMKALIRVLONFSFKCKETOIPLKLSIGLLQPEKPVVLKVESRDGVVSGA 481
DB 445 GMEFALNMKALIRVLONFSFKCKETOIPLKLSIGLLQPEKPVVLKVESRDGVVSGA 504

RESULT 6
US-10-732-923-1079
; Sequence 1079, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15 (52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 1079
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Macaca faecicularis
US-10-732-923-1079

Query Match 93.3%; Score 2372; DB 17; Length 503;
Best Local Similarity 93.9%; Pred. No. 5.9e-203;
Matches 450; Conservative 18; Mismatches 11; Indels 0; Gaps 0;

QY 3 YGTHSHGLFKKLGIPGTPPLPFLGNILSYHKGFCMFDECHKKYKGVGFDGQOQVLA 62
DB 25 YGTHSHGLFKKLGIPGTPPLPFLGNILSYHKGFWTDMECYKKYKGVGFDGQOQVLA 84
QY 63 TDDPMIKTVLVKCYSVFTNRRPFGVGFPMKSAISIAEDEEMKRLSLSPFTSGKKE 122
DB 85 TDDPMIKTVLVKCYSVFTNRRPFGVGFPMKSAISIAEDEEMKRLSLSPFTSGKKE 144
QY 123 MPEIIAOGDVLYRNLRREAEFGKPVTLKDVGAYSMDVITSTSGVNIIDSLNPDQPV 182
DB 145 MPEIIAOGDVLYRNLRREAEFGKPVTLKDVGAYSMDVITSTSGVNIIDSLNPDQPV 204
QY 183 ENTKKLARDFLDPFLSLITVPFPLIPILEVNICVFPREVTNPLKRSYKRMKESRLBDT 242
DB 205 ENTKKLARDFLDPFLSLITVPFPLIPILEVNICVFPREVTNPLKRSYKRMKESRLBDT 264
QY 243 QKRVDFLOLMIDSQNSKTESHKAISDELVAOSIIIFAGYETTSSVLSFIMELATH 302
DB 265 QKRVDFLOLMIDSQNSKTESHKAISDELVAOSIIIFAGYETTSSVLSFIMELATH 324
QY 303 PDVQOKLOEIDAVLPNKAPPTVDVLOMEYLDVMVNETLRPLFPIAMLERVCKKDOVEI 362
DB 325 PDVQOKLOEIDAVLPNKAPPTVDVLOMEYLDVMVNETLRPLFPIAMLERVCKKDOVEI 384
QY 363 GMEFIPKGVVMI PSYALHBDPKWTEPEKFLPERFSKKNKONIDPIYITPFGSGPRNCIG 422
DB 385 GMEFIPKGVVMI PSYALHBDPKWTEPEKFLPERFSKKNKONIDPIYITPFGSGPRNCIG 444
QY 423 MRPALNMKALIRVLONFSFKCKETOIPLKLSIGLLQPEKPVVLKVESRDGVVSGA 481
DB 445 MRPALNMKALIRVLONFSFKCKETOIPLKLSIGLLQPEKPVVLKVESRDGVVSGA 503
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RESULT 7
US-09-957-997-3
; Sequence 3, Application US/09957997
; Patent No. US20020150915A1
; GENERAL INFORMATION:
; APPLICANT: Berkenstein, Anders
; APPLICANT: Blomquist, Patrik
; APPLICANT: Berglund, Johan
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-046001
; CURRENT APPLICATION NUMBER: US/09/957,997
; PRIOR FILING DATE: 2001-09-21
; EARLIER APPLICATION NUMBER: SE 0003393-6
; EARLIER FILING DATE: 2000-09-22
; EARLIER APPLICATION NUMBER: 60/238,895
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-957-997-3

Query Match 87.8%; Score 2233; DB 9; Length 503;
Best Local Similarity 88.7%; Pred. No. 1.6e-190;
Matches 425; Conservative 27; Mismatches 27; Indels 0; Gaps 0;

QY 3 YGTHSHGLFKKLGIPGTPPLPFLGNILSYHKGFCMFDECHKKYKGVGFDGQOQVLA 62
DB 25 YGTHSHGLFKKLGIPGTPPLPFLGNILSYHKGFWTDMECYKKYKGVGFDGQOQVLA 84
QY 63 TDDPMIKTVLVKCYSVFTNRRPFGVGFPMKSAISIAEDEEMKRLSLSPFTSGKKE 122
DB 85 TDDPMIKTVLVKCYSVFTNRRPFGVGFPMKSAISIAEDEEMKRLSLSPFTSGKKE 144
QY 123 MPEIIAOGDVLYRNLRREAEFGKPVTLKDVGAYSMDVITSTSGVNIIDSLNPDQPV 182
DB 145 MPEIIAOGDVLYRNLRREAEFGKPVTLKDVGAYSMDVITSTSGVNIIDSLNPDQPV 204
QY 183 ENTKKLARDFLDPFLSLITVPFPLIPILEVNICVFPREVTNPLKRSYKRMKESRLBDT 242
DB 205 ENTKKLARDFLDPFLSLITVPFPLIPILEVNICVFPREVTNPLKRSYKRMKESRLBDT 264
QY 243 QKRVDFLOLMIDSQNSKTESHKAISDELVAOSIIIFAGYETTSSVLSFIMELATH 302
DB 265 QKRVDFLOLMIDSQNSKTESHKAISDELVAOSIIIFAGYETTSSVLSFIMELATH 324
QY 303 PDVQOKLOEIDAVLPNKAPPTVDVLOMEYLDVMVNETLRPLFPIAMLERVCKKDOVEI 362
DB 325 PDVQOKLOEIDAVLPNKAPPTVDVLOMEYLDVMVNETLRPLFPIAMLERVCKKDOVEI 384
QY 363 GMEFIPKGVVMI PSYALHBDPKWTEPEKFLPERFSKKNKONIDPIYITPFGSGPRNCIG 422
DB 385 GMEFIPKGVVMI PSYALHBDPKWTEPEKFLPERFSKKNKONIDPIYITPFGSGPRNCIG 444
QY 423 MRPALNMKALIRVLONFSFKCKETOIPLKLSIGLLQPEKPVVLKVESRDGVVSGA 481
DB 445 MRPALNMKALIRVLONFSFKCKETOIPLKLSIGLLQPEKPVVLKVESRDGVVSGA 503

RESULT 8
US-10-626-686-66
; Sequence 66, Application US/10626686
; Publication No. US20050074842A1
; GENERAL INFORMATION:
; APPLICANT: Sekine, Shingo
; APPLICANT: Kimura, Tomoko
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE
; FILE REFERENCE: GIN-6706CPUS
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CURRENT APPLICATION NUMBER: US/10/626,686
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US/09/445,258A
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: PCT/US98/02445
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: JP 9-144948
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 66
LENGTH: 499
TYPE: PRT
ORGANISM: Macaca fascicularis
US-10-626-686-66

Query Match      79.1%; Score 2011.5; DB 17; Length 499;
Best Local Similarity 82.0%; Pred. No. 9.7e-17;
Matches 393; Conservative 16; Mismatches 9; Indels 61; Gaps 2;

QY 3 YGTHSHGIFKKLGIIPGPTPLPLGNILSYHKGFCMFMECHKKTKGKVGFTDGOQPVLA1 62
DB 82 YGTHSHGIFKKLGIIPGPTPLPLGNILSYHKGFCMFMECHKKTKGKVGFTDGOQPVLA1 140
QY 63 TDPDMIKTVLVKCEYVFTNRPRPGVGFMSAISIADEDEWKRSLSPFTSGKLKE 122
DB 141 TDPDMIKTVLVKCEYVFTNRPRPGVGFMSAISIADEDEWKRSLSPFTSGKLKE 200
QY 123 MWPIIAQYGVLVNLRREAEATGKPVTLKDFGAYSMVDITSTSGVINDSLNPPDPFV 182
DB 201 MWPIIAQYGVLVNLRREAEATGKPVTLKDFGAYSMVDITSTSGVINDSLNPPDPFV 260
QY 183 ENTCKLARPDLDPPPLSTITVPPLIPLIEVLANICVPPREVTNLRKSVKMKSRLEDT 242
DB 261 ENTCKLARPDLDPPPLSTITVPPLIPLIEVLANICVPPREVTNLRKSVKMKSRLEDT 320
QY 243 QKRVDFLOLMIDSONSKETESHKALSDLEVAOSIIFIFAGYETTSVLSFIWEYLATH 302
DB 321 QKRVDFLOLMIDSONSKETESHKALSDLEVAOSIIFIFAGYETTSVLSFIWEYLATH 380
QY 303 PDVQOQLOEIDAVLPNKAAPTVDVLOMEYLDVNVNLTLPFIAMLERVCKKQVEIN 362
DB 381 PDVQOQLOEIDAVLPNKAAPTVDVLOMEYLDVNVNLTLPFIAMLERVCKKQVEIN 415
QY 363 GMRPIKGVVWVMSYALHRDPKYTEPEKFLPERFSKKNKNDIDPIYTPPGSGPRNCIG 422
DB 416 -----SKKNNDNDIDPIYTPPGSGPRNCIG 440
QY 423 MRFALMMKALIRVLQNFSPKCKETOIPLKLSIGLLOPEKPVVLKVESRQTVSGA 481
DB 441 MRFALMMKALIRVLQNFSPKCKETOIPLKLSIGLLOPEKPVVLKVESRQTVSGA 499

RESULT 9
US-10-274-694-7
Sequence 7, Application US/10274694
Publication No. US20030143589A1
GENERAL INFORMATION:
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BRUNS, Christopher M.
APPLICANT: DAS, Debopriya
APPLICANT: DING, Li
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: GANDHI, Ameena R.
APPLICANT: HAFALIA, April J.A.
APPLICANT: KEARNEY, Liam
APPLICANT: KHAN, Farrah A.
APPLICANT: LAL, Preeti G.
APPLICANT: LEE, Ernestine A.
APPLICANT: LU, Dying Alina M.
APPLICANT: NGUYEN, Daniel B.
APPLICANT: PATTERSON, Chandra S.
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APPLICANT: RAMKUNAR, Javalaxmi
APPLICANT: RING, Huijun Z.
APPLICANT: SANJANWALA, Madhusudan M.
APPLICANT: TANG, Y. Tom
APPLICANT: THANGAVELU, Kavitha
APPLICANT: THORNTON, Michael B.
APPLICANT: TRIBOLEY, Catherine M.
APPLICANT: MALIA, Narinder K.
APPLICANT: XU, Yuming
APPLICANT: YANG, Junming
APPLICANT: YAO, Monique G.
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REFERENCE: PI-0151 USA
CURRENT APPLICATION NUMBER: US/10/274,694
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 60/221,837
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/220,037
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 60/218,948
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US01/21324
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/216,804
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PERL Program
SEQ ID NO 7
LENGTH: 502
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030143589A1 7476298CD1
US-10-274-694-7

Query Match      77.0%; Score 1958; DB 14; Length 502;
Best Local Similarity 76.0%; Pred. No. 5.9e-166;
Matches 364; Conservative 52; Mismatches 63; Indels 0; Gaps 0;

QY 2 AYGTHSHGIFKKLGIIPGPTPLPLGNILSYHKGFCMFMECHKKTKGKVGFTDGOQPVLA 61
DB 23 SYGTHSHGIFKKLGIIPGPTPLPLGNILSYHKGFCMFMECHKKTKGKVGFTDGOQPVLA 82
QY 62 ITDPMIKTVLVKCEYVFTNRPRPGVGFMSAISIADEDEWKRSLSPFTSGKLK 121
DB 83 IMPDMIKTVLVKCEYVFTNRPRPGVGFMSAISIADEDEWKRSLSPFTSGKLK 142
QY 122 EMVPIIAQYGVLVNLRREAEATGKPVTLKDFGAYSMVDITSTSGVINDSLNPPDPF 181
DB 143 EMVPIIAQYGVLVNLRREAEATGKPVTLKDFGAYSMVDITSTSGVINDSLNPPDPF 202
QY 182 VENTCKLARPDLDPPPLSTITVPPLIPLIEVLANICVPPREVTNLRKSVKMKSRLEDT 241
DB 203 LKMKKQLKIDPDLPLPLISLFPFLPVFEALNIGLFPDQVHFKNSIERKESRLKD 262
QY 242 TOKRVDFLOLMIDSONSKETESHKALSDLEVAOSIIFIFAGYETTSVLSFIWEYLATH 301
DB 263 KQKRVDFLOLMIDSONSKETESHKALSDLEVAOSIIFIFAGYETTSVLSFIWEYLATH 322
QY 302 HPVQOQLOEIDAVLPNKAAPTVDVLOMEYLDVNVNLTLPFIAMLERVCKKQVEIN 361
DB 323 HPVQOQLOEIDAVLPNKAAPTVDVLOMEYLDVNVNLTLPFIAMLERVCKKQVEIN 382
QY 362 NGMRPIKGVVWVMSYALHRDPKYTEPEKFLPERFSKKNKNDIDPIYTPPGSGPRNCIG 421
DB 383 NGMRPIKGVVWVMSYALHRDPKYTEPEKFLPERFSKKNKNDIDPIYTPPGSGPRNCIG 442
QY 422 MRFALMMKALIRVLQNFSPKCKETOIPLKLSIGLLOPEKPVVLKVESRQTVSGA 480
DB 443 MRFALMMKALIRVLQNFSPKCKETOIPLKLSIGLLOPEKPVVLKVESRQTVSGA 501
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RESULT 10
US-10-332-448-7
; Sequence 7, Application US/10332448
; Publication No. US20040253588A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; BAUGHN, Mariah R.;
; APPLICANT: CHRISTOPHER M.; DAS, Debopriya Das;
; APPLICANT: BRUNS, Christopher M.; S. GANDHI, Ameena R.;
; APPLICANT: DING, Li; ELLIOTT, Vicki S.;
; APPLICANT: HAFALIA, April; KERNERT, Liam; KHAN, Farrah A.;
; APPLICANT: LAL, Preeti; LEE, Ernestine A.; LU, Dyoung Alina M.;
; APPLICANT: LU, Yan; DANNIEL, Nguyen B.; ARVITU, Chandra S.;
; APPLICANT: RAMKUMAR, Jayalaxmi; RING, Huijun Z.;
; APPLICANT: SAMJANWALA, Madhu S.; TANG, Y. Tom;
; APPLICANT: THANGAVELU, Kavitha; THORNTON, Michael;
; APPLICANT: TRIBOULET, Catherine M.; WALIA, Natinder K.;
; APPLICANT: XU, Yuming; YANG, Junning; YAO, Monique G.; YUE, Henry
; TITLE OF INVENTION: Drug Metabolizing Enzymes
; FILE REFERENCE: PI-0151 USN
; CURRENT APPLICATION NUMBER: US/10/332,448
; FILE REFERENCE: PI-0151 USN
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/216,804
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/218,948
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/220,037
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/221,837
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7476298CD1
US-10-332-448-7

Query Match 77.0%; Score 1958; DB 16; Length 502;
Best Local Similarity 76.0%; Pred. No. 5.9e-166;
Matches 364; Conservative 52; Mismatches 63; Indels 0; Gaps 0;
QY 2 AYCSTHGLFKKLGIPGPPPLPFLGNLSYHKGFCMFDECHKKYGVGGQGVLA 61
DB 23 SYGTHSHKLFKKGIPGPPPLPFLGTLFLYLRGLMNFDECHKKYGVGGQGVLA 82
QY 62 ITDPDMIKTVLVKCYSVFTNRRPFGVGFMSAISIAEDDEWKRLRLSPFTSGKL 121
DB 83 IMPDMIKTVLVKCYSVFTNRRPFGVGFMSAISIAEDDEWKRLRLSPFTSGKL 142
QY 122 EMVPIIAQGVGVVLRNLRREAEFGKPVTLKDVFGAYSMDVITSTSGVNIIDSNPDP 181
DB 143 EMVPIISQCGDMVLRSLRQEAENSKSINLKDFFGAYTMVITGTLFGVNIIDSNPDP 202
QY 182 VENTKGLRDFLDPFPLSLTVRPLPILEVLNICVPRREVTNPLKSKVKMKESRLD 241
DB 203 LKMKKLLKLDLDFPFLSLTVRPLPILEVLNICVPRREVTNPLKSKVKMKESRLD 262
QY 242 TQGRVDFQLMDLSDNSKTESHKAISDELEVAOSIIIFAGYETTSVLSIMTELAT 301
DB 263 KQHRVDFPQOMIDSONSKTESHKAISDELEVAOSIIIFAGYETTSVLSIMTELAT 322
QY 302 HPDVQKLOEIDAVLPNKAPPTYDVLQMEYLDVNVNELLRLFPAMLERVCKDOVEI 361
DB 323 HPDVQKLOEIDAVLPNKAPPTYDVLQMEYLDVNVNELLRLFPAMLERVCKDOVEI 382
QY 362 NGMFIRKGVVVMIPSYALHDPKWTPEPEKFLPERPSKKKNKONIDYIYTPFGSGRNCI 421
DB 383 NGVFIRKGVVVMIPSYALHDPKWTPEPEKFLPERPSKKKNKONIDYIYTPFGSGRNCI 442
QY 422 GKRFALNMKGLAIRVLQNFSPKCKETOIPLKLSIGLLQPEKPVVLKVESDGTGVS 480

DB 443 GKRFALNMKGLAIRVLQNFSPKCKETOIPLKLSIGLLQPEKPVVLKVESDGTGVS 501
RESULT 11
US-10-007-814-2
; Sequence 2, Application US/10007814
; Publication No. US20020160479A1
; GENERAL INFORMATION:
; APPLICANT: Wojnowski, Leszek
; APPLICANT: Gellner, Klaus
; APPLICANT: Eisele, Regina
; TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
; FILE REFERENCE: 310115.403D1
; CURRENT APPLICATION NUMBER: US/10/007,814
; CURRENT FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-814-2

Query Match 77.0%; Score 1957; DB 13; Length 503;
Best Local Similarity 76.2%; Pred. No. 7.3e-166;
Matches 364; Conservative 51; Mismatches 63; Indels 0; Gaps 0;
QY 3 YGTHSHGLFKKLGIPGPPPLPFLGNLSYHKGFCMFDECHKKYGVGGQGVLA 62
DB 25 YGTHSHKLFKKGIPGPPPLPFLGTLFLYLRGLMNFDECHKKYGVGGQGVLA 84
QY 63 ITDPDMIKTVLVKCYSVFTNRRPFGVGFMSAISIAEDDEWKRLRLSPFTSGKL 122
DB 85 IMPDMIKTVLVKCYSVFTNRRPFGVGFMSAISIAEDDEWKRLRLSPFTSGKL 144
QY 122 EMVPIIAQGVGVVLRNLRREAEFGKPVTLKDVFGAYSMDVITSTSGVNIIDSNPDP 182
DB 145 EMVPIISQCGDMVLRSLRQEAENSKSINLKDFFGAYTMVITGTLFGVNIIDSNPDP 204
QY 183 ENTKGLRDFLDPFPLSLTVRPLPILEVLNICVPRREVTNPLKSKVKMKESRLD 242
DB 205 KMKKLLKLDLDFPFLSLTVRPLPILEVLNICVPRREVTNPLKSKVKMKESRLD 264
QY 243 QGRVDFQLMDLSDNSKTESHKAISDELEVAOSIIIFAGYETTSVLSIMTELAT 302
DB 265 QGRVDFPQOMIDSONSKTESHKAISDELEVAOSIIIFAGYETTSVLSIMTELAT 324
QY 303 PVOQKLOEIDAVLPNKAPPTYDVLQMEYLDVNVNELLRLFPAMLERVCKDOVEI 362
DB 325 PVOQKLOEIDAVLPNKAPPTYDVLQMEYLDVNVNELLRLFPAMLERVCKDOVEI 384
QY 363 GMFIRKGVVVMIPSYALHDPKWTPEPEKFLPERPSKKKNKONIDYIYTPFGSGRNCI 422
DB 385 GMFIRKGVVVMIPSYALHDPKWTPEPEKFLPERPSKKKNKONIDYIYTPFGSGRNCI 444
QY 422 MKRFALNMKGLAIRVLQNFSPKCKETOIPLKLSIGLLQPEKPVVLKVESDGTGVS 480
DB 445 MKRFALNMKGLAIRVLQNFSPKCKETOIPLKLSIGLLQPEKPVVLKVESDGTGVS 502
RESULT 12
US-10-112-944-432
; Sequence 432, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Gezi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.

APPLICANT: Wang, Jian-Rui
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Malabika
APPLICANT: Wang, Dunrui
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Zhilwei
TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
TITLE OF INVENTION: Secreted Polypeptides
FILE REFERENCE: 805A
CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SOFTWARE: pc_fl_genes Version 5.0
SEQ ID NO 432
LENGTH: 503
TYPE: PRT
ORGANISM: Homo sapiens
US-10-112-944-432

Query Match 76.9%; Score 1956; DB 15; Length 503;
Best Local Similarity 76.2%; Pred. No. 8.9e-166;

Matches 364; Conservative 50; Mismatches 64; Indels 0; Gaps 0;

3 YGTHSHGLFKKGIKGPPTLPFLGNILSYHKGFCMDECHKYKGYMGFYDGOQPLAI 62
25 YGTHSHGLFKKGIKGPPTLPFLGNILSYHKGFCMDECHKYKGYMGFYDGOQPLAI 84
63 TDPDMITVLYKCEYVFTNRPRPGVGFMSAISIADEDEMRKRLSLSPFTSGLKE 122
85 MDPDMITVLYKCEYVFTNRPRPGVGFMSAISIADEDEMRKRLSLSPFTSGLKE 144
123 MDPDMITVLYKCEYVFTNRPRPGVGFMSAISIADEDEMRKRLSLSPFTSGLKE 182
145 MDPDMITVLYKCEYVFTNRPRPGVGFMSAISIADEDEMRKRLSLSPFTSGLKE 204
183 ENTGKLRPFLDPLPFLSTIVFPFLPILVLANICVPPREVYNFLRKSVMKESRLDET 242
205 KMKKGLKLPFLDPLPFLSTIVFPFLPILVLANICVPPREVYNFLRKSVMKESRLDET 264
243 QKRVDPFLQMLDSQNSKETESHKALSDLEVAOSIIFPAGVETTSVLSPIWELATH 302
265 QKRVDPFLQMLDSQNSKETESHKALSDLEVAOSIIFPAGVETTSVLSPIWELATH 324
303 PDVQOKLQSEIDAVLPKAPPTVTVLQMEYLDVNVNETHLPPIAMRLERVKCKOIEIN 362
325 PDVQOKLQSEIDAVLPKAPPTVTVLQMEYLDVNVNETHLPPIAMRLERVKCKOIEIN 384
363 GMFIPKGVVMIPSYALHDPKWTBEPKFLPERFSKKNKONIDPIYITPFGSGPRNCIG 422
385 GVFIPIKGLAVWPIYALHDPKWTBEPKFLPERFSKKNKONIDPIYITPFGSGPRNCIG 444
423 MRPLANMKALALIRVLONFSFKPKETQIPKLSLGLLOPEKPVVLKVESRDGTSG 480
445 MRPLANMKALALIRVLONFSFKPKETQIPKLSLGLLOPEKPVVLKVESRDGTSG 502

RESULT 13

US-10-007-814-4
Sequence 4, Application US/10007814
Publication No. US20020160479A1
GENERAL INFORMATION:
APPLICANT: Mojonewski, Leszek
APPLICANT: Gellner, Klaus
APPLICANT: Elsbelt, Regina
TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
FILE REFERENCE: 310115.401D1
CURRENT APPLICATION NUMBER: US/10/007,814
CURRENT FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 504
TYPE: PRT
ORGANISM: Homo sapiens
US-10-007-814-4

Query Match 76.6%; Score 1946.5; DB 13; Length 504;
Best Local Similarity 76.0%; Pred. No. 6.3e-165;

Matches 364; Conservative 51; Mismatches 63; Indels 1; Gaps 1;

3 YGTHSHGLFKKGIKGPPTLPFLGNILSYHKGFCMDECHKYKGYMGFYDGOQPLAI 62
25 YGTHSHGLFKKGIKGPPTLPFLGNILSYHKGFCMDECHKYKGYMGFYDGOQPLAI 84
63 TDPDMITVLYKCEYVFTNRPRPGVGFMSAISIADEDEMRKRLSLSPFTSGLKE 122
85 MDPDMITVLYKCEYVFTNRPRPGVGFMSAISIADEDEMRKRLSLSPFTSGLKE 144
123 MDPDMITVLYKCEYVFTNRPRPGVGFMSAISIADEDEMRKRLSLSPFTSGLKE 182
145 MDPDMITVLYKCEYVFTNRPRPGVGFMSAISIADEDEMRKRLSLSPFTSGLKE 204
183 ENTGKLRPFLDPLPFLSTIVFPFLPILVLANICVPPREVYNFLRKSVMKESRLDET 242
205 KMKKGLKLPFLDPLPFLSTIVFPFLPILVLANICVPPREVYNFLRKSVMKESRLDET 264
243 QKRVDPFLQMLDSQNSKETESHKALSDLEVAOSIIFPAGVETTSVLSPIWELATH 302
265 QKRVDPFLQMLDSQNSKETESHKALSDLEVAOSIIFPAGVETTSVLSPIWELATH 324
303 PDVQOKLQSEIDAVLPKAPPTVTVLQMEYLDVNVNETHLPPIAMRLERVKCKOIEIN 362
325 PDVQOKLQSEIDAVLPKAPPTVTVLQMEYLDVNVNETHLPPIAMRLERVKCKOIEIN 384
363 GMFIPKGVVMIPSYALHDPKWTBEPKFLPERFSKKNKONIDPIYITPFGSGPRNCI 421
385 GVFIPIKGLAVWPIYALHDPKWTBEPKFLPERFSKKNKONIDPIYITPFGSGPRNCI 444
422 GMFIPKGVVMIPSYALHDPKWTBEPKFLPERFSKKNKONIDPIYITPFGSGPRNCI 480
445 GMFIPKGVVMIPSYALHDPKWTBEPKFLPERFSKKNKONIDPIYITPFGSGPRNCI 503

RESULT 14

US-10-274-694-16
Sequence 16, Application US/10274694
Publication No. US20030143589A1
GENERAL INFORMATION:
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BRUNS, Christopher M.
APPLICANT: DAS, Deepriya
APPLICANT: DING, Li
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: GANDHI, Ameena R.
APPLICANT: HAFALIA, April J.A.
APPLICANT: KEARNEY, Liam
APPLICANT: KHAN, Farrah A.
APPLICANT: LAL, Preeti G.
APPLICANT: LEE, Ernestine A.


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Db      323 MYELATHPDVQOKLOEELIDAVLPNKAPVTYDALVQMEYLDNVNETHLRFVVSRTVRC 382
Qy      356 KKDVEINGMFTLPKGVVWMIIPSYALHRDPKWTBEPKFLPERFSKKNKNDIDPIYTPFGS 415
Db      383 KKDIEINGVFLPKGLAVWVPYIALHDPKWTBEPKFCPERFSKKNKDSIDLRYIPFGA 442
Qy      416 GPRNCIGWRFPALMMKCLIRVLONFSFPCCKETOIPIKLSLGGILOPEKPVTLKVESRD 475
Db      443 GPRNCIGWRFPALMMKCLIRVLONFSFPCCKETOIPIKLSLGGILOPEKPVTLKVESRD 502
Qy      476 GTVSG 480
Db      503 GTSG 507

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Search completed: July 8, 2005, 14:30:06
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